5-22-2007

PSEUDOMONAS AVR AND HOP PROTEINS, THEIR ENCODING NUCLEIC ACIDS, AND USE THEREOF

James R. Alfano
Lincoln, NE

Alan Collmer
Ithaca, NY

Samuel W. Cartinhour
Ithaca, NY

David J. Schneider
Trumansburg, NY

US007220583B2

(12) **United States Patent**
Alfano et al.

(10) **Patent No.: US 7,220,583 B2**
(45) **Date of Patent: May 22, 2007**

(54) ***PSEUDOMONAS* AVR AND HOP PROTEINS, THEIR ENCODING NUCLEIC ACIDS, AND USE THEREOF**

(75) Inventors: **James R. Alfano**, Lincoln, NE (US); **Alan Collmer**, Ithaca, NY (US); **Samuel W. Cartinhour**, Ithaca, NY (US); **David J. Schneider**, Trumansburg, NY (US)

(73) Assignees: **Cornell Research Foundation, Inc.**, Ithaca, NY (US); **The Board of Regents of the University of Nebraska**, Lincoln, NE (US); **The United States of America, as Represented by the Secretary of Agriculture**, Washington, DC (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 12 days.

(21) Appl. No.: **10/365,742**

(22) Filed: **Feb. 12, 2003**

(65) **Prior Publication Data**

US 2003/0204868 A1 Oct. 30, 2003

Related U.S. Application Data

(60) Provisional application No. 60/356,408, filed on Feb. 12, 2002, provisional application No. 60/380,185, filed on May 10, 2002.

(51) **Int. Cl.**

C12N 9/12	(2006.01)
C12N 15/00	(2006.01)
C12N 15/82	(2006.01)
C12P 21/06	(2006.01)
C07H 21/04	(2006.01)
C12Q 1/48	(2006.01)
A61K 38/52	(2006.01)

(52) **U.S. Cl.** **435/375**; 435/15; 435/69.1; 435/320.1; 435/194; 424/94.5; 800/279; 800/280; 800/292; 800/293; 536/23.2

(58) **Field of Classification Search** 424/94.1, 424/94.5; 435/252.3, 254.2, 325, 419, 320.1, 435/468, 471, 375, 194, 69.1, 15; 536/23.1; 800/3, 4, 278

See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,342,654 B1 1/2002 Li et al.

FOREIGN PATENT DOCUMENTS

WO WO 99/07207 2/1999

OTHER PUBLICATIONS

Seffernick et al., Melamine deaminase and atrazine chlorohydrolase: 98 percent identical but functionally different. J Bacteriol. 183(8): 2405-2410, 2001.*

Houslay et al., Cell-type specific integration of cross-talk between extracellular signal-regulated kinase and cAMP signaling. Mol Pharmacol. 58(4): 659-668, 2000.*

Whisstock et al., Prediction of protein function from protein sequence and structure. Q Rev Biophys. 36(3): 307-340, 2003.*

Collmer et al., "*Pseudomonas syringae* Hrp Type III Secretion System and Effector Proteins," *PNAS* 97(16):8770-8777 (2000).

Alfano et al., "The *Pseudomonas syringae* Hrp Pathogenicity Island has a Tripartite Mosaic Structure Composed of a Cluster of Type III Secretion Genes Bounded by Exchangeable Effector and Conserved Effector Loci That Contribute to Parasitic Fitness and Pathogenicity in Plants," *PNAS* 97(9):4856-4861 (2000).

Fouts et al., "Genomewide Identification of *Pseudomonas syringae* pv. Tomato DC3000 Promoters Controlled by the HrpL Alternative Sigma Factor," *PNAS* 99(4):2275-2280 (2002), with supplemental material available online at www.pnas.org.

Petnicki-Ocwieja et al., "Genomewide Identification of Proteins Secreted by the Hrp Type III Protein Secretion System of *Pseudomonas syringae* pv. Tomato DC3000," *PNAS* 99(11):7652-7657 (2002), with supplemental material available online at www.pnas.org.

Zwiesler-Vollick et al., "Identification of Novel *hrp*-regulated Genes through Functional Genomic Analysis of the *Pseudomonas syringae* pv. *Tomato* DC3000 Genome," *Molecular Microbiology* 45(5):1207-1218 (2002).

Guttman et al., "A Functional Screen for the Type III (hrp) Secretome of the Plant Pathogen *Pseudomonas syringae," Science*, 295(5560):1722-1726 (2002).

Vinatzer et al., GenBank Accession No. AF458398, (2002).

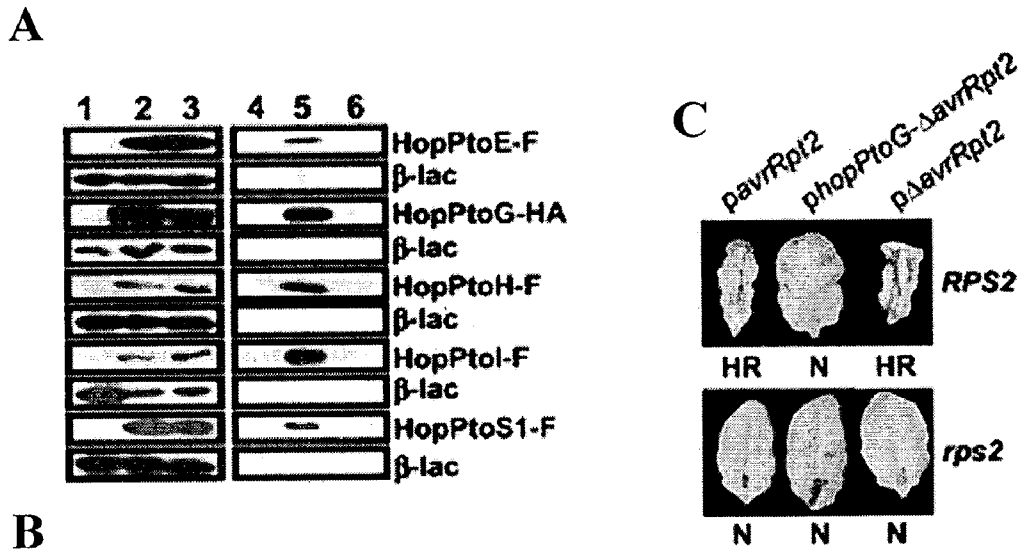
* cited by examiner

Primary Examiner—Rebecca E. Prouty
Assistant Examiner—Ganapathirama Raghu
(74) *Attorney, Agent, or Firm*—Nixon Peabody LLP

(57) **ABSTRACT**

One aspect of the present invention relates to isolated nucleic acid molecules encoding avirulence proteins or polypeptides of *Pseudomonas syringae* pv. *syringae* DC 3000, or nucleic acid molecules which are complementary thereto. Expression vectors, host cells, and transgenic plants which include the DNA molecules of the present invention are also disclosed. Another aspect relates to the isolated proteins or polypeptides and compositions containing the same. The various nucleic acid molecules and proteins of the present invention can be used to impart disease resistance to a plant, make a plant hypersusceptible to colonization by nonpathogenic bacteria, modify a metabolic pathway in a cell, cause eukaryotic cell death and treat a cancerous condition, as well as inhibit programmed cell death.

5 Claims, 7 Drawing Sheets


A
1 2 3 4 5 6
HopPtoE-F
β-lac
HopPtoG-HA
β-lac
HopPtoH-F
β-lac
HopPtoI-F
β-lac
HopPtoS1-F
β-lac
B
1 2 3 4 5 6
HopPtoL-F
β-lac
HopPtoS2-F
β-lac
C
pavrRpt2
phopPtoG-ΔavrRpt2
pΔavrRpt2
RPS2
HR N HR
rps2
N N N

Figures 1A-C

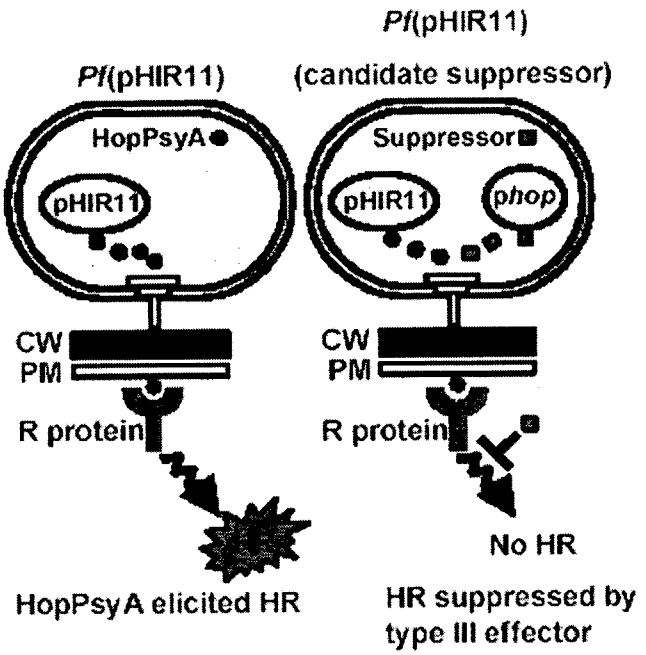


Figure 2A

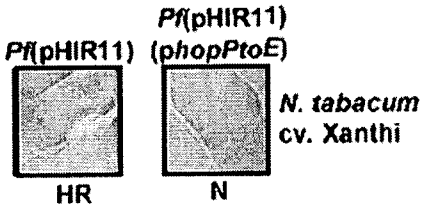


Figure 2B

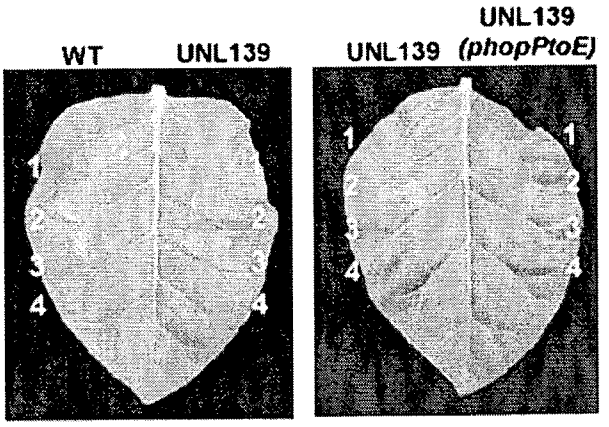


Figure 2C

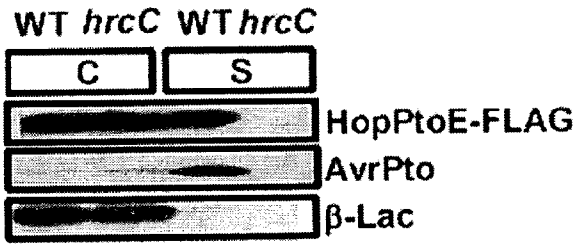


Figure 3A

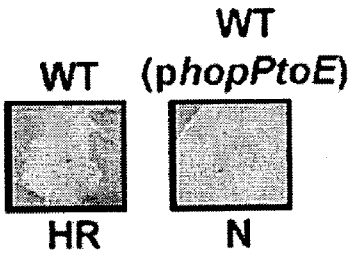


Figure 3B

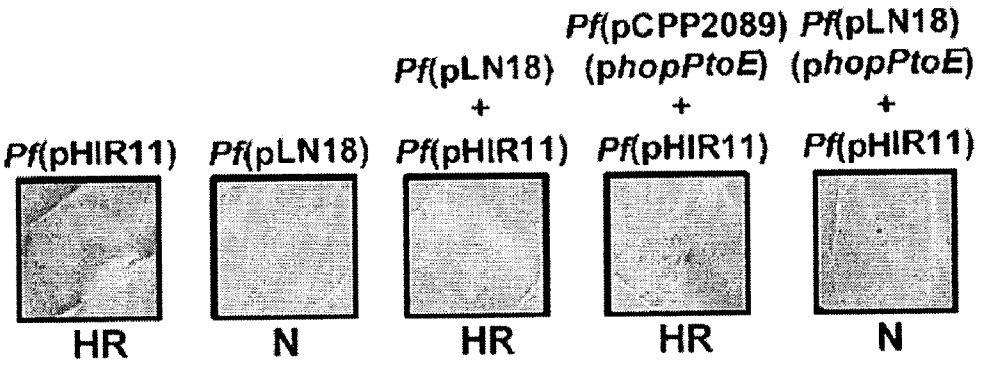


Figure 3C

Effector	$AvrPphE_{Pto}$	$AvrPpiB1_{Pto}$	$AvrPto$	AvrPtoB	HopPtoB	HopPtoC	HopPtoD1	HopPtoD2	HopPtoE	HopPtoF	HopPtoG	HopPtoH	HopPtoI	HopPtoJ	HopPtoK	HopPtoL	HopPtoS1	HopPtoS2	HopPtoT
Suppression	y	y	n	y	n	n	y*	n	y	y	n	n	n	n	y*	n	n	n	n

Figure 4A

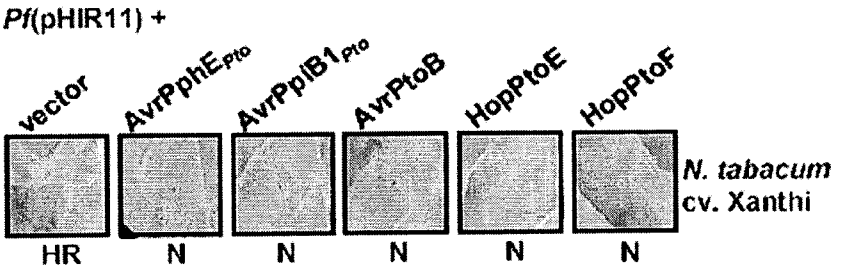


Figure 4B

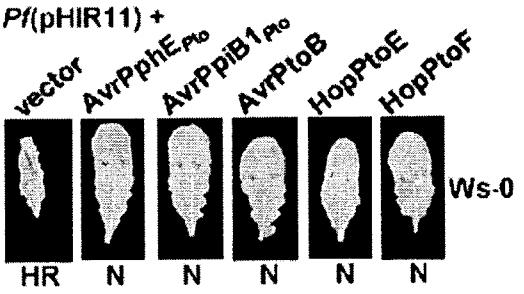


Figure 4C

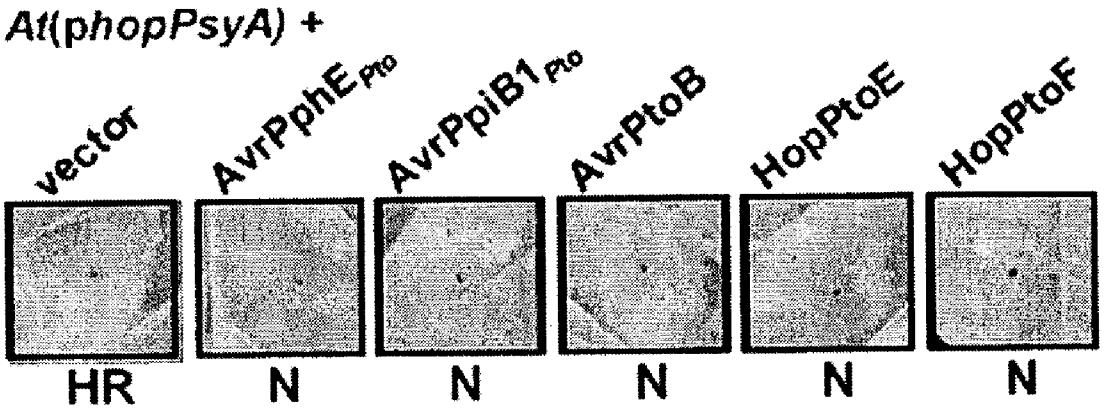


Figure 5A

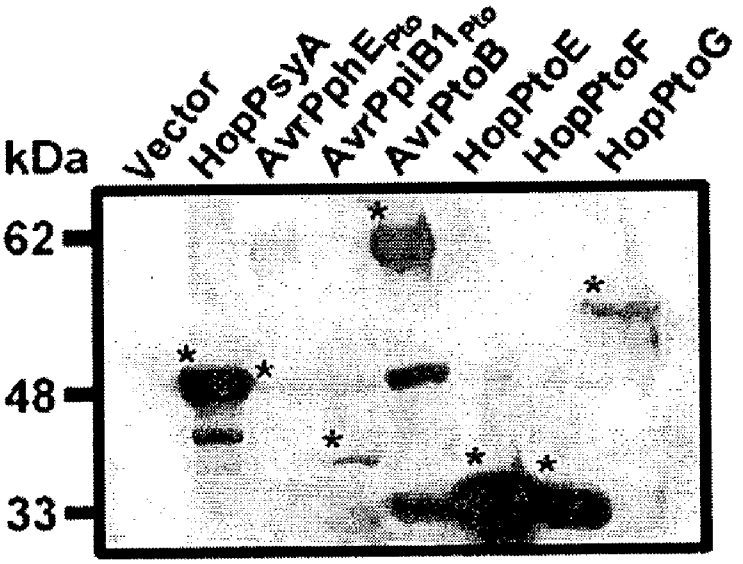


Figure 5B

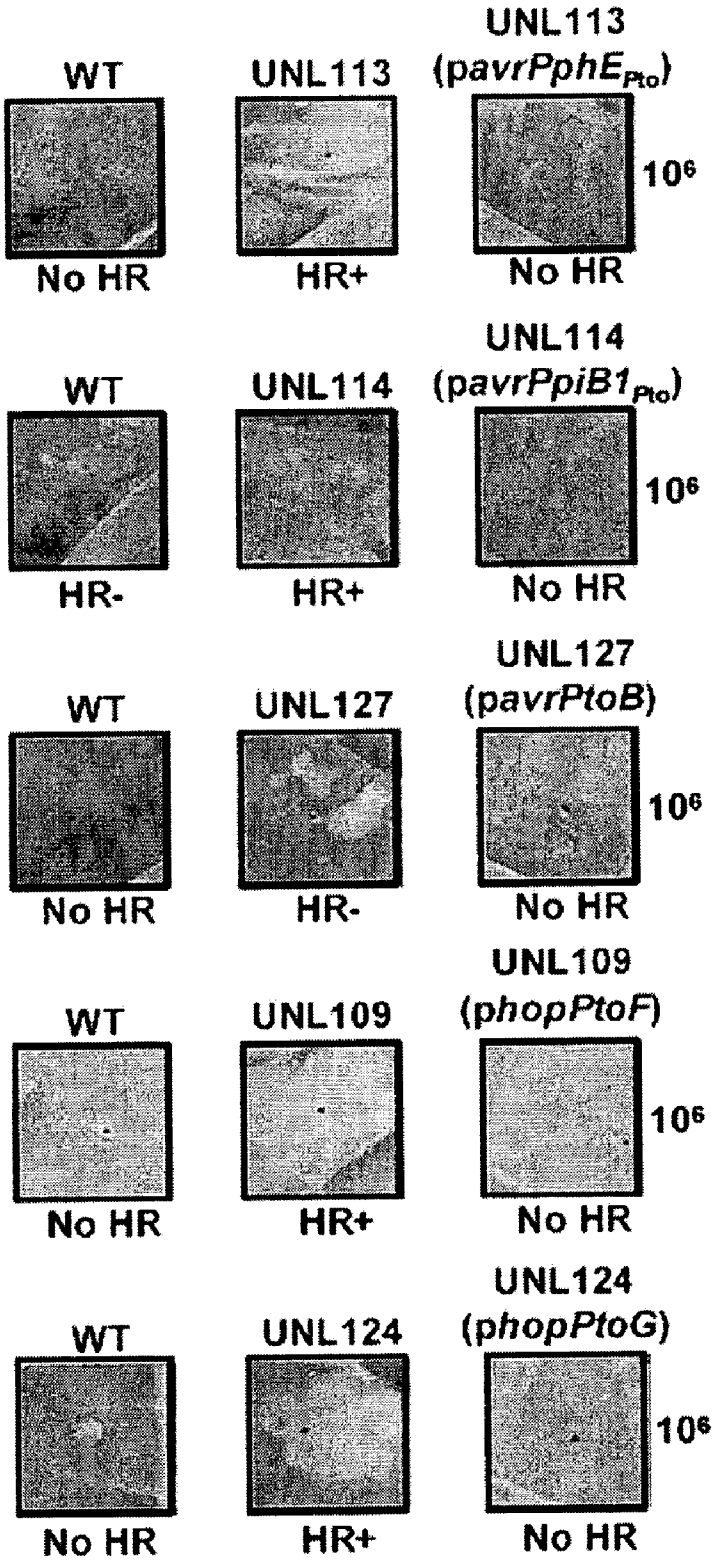

WT
UNL113
UNL113 (pavrPphE$_{Pto}$)
10^6
No HR
HR+
No HR
WT
UNL114
UNL114 (pavrPpiB1$_{Pto}$)
10^6
HR-
HR+
No HR
WT
UNL127
UNL127 (pavrPtoB)
10^6
No HR
HR-
No HR
WT
UNL109
UNL109 (phopPtoF)
10^6
No HR
HR+
No HR
WT
UNL124
UNL124 (phopPtoG)
10^6
No HR
HR+
No HR

Figure 6

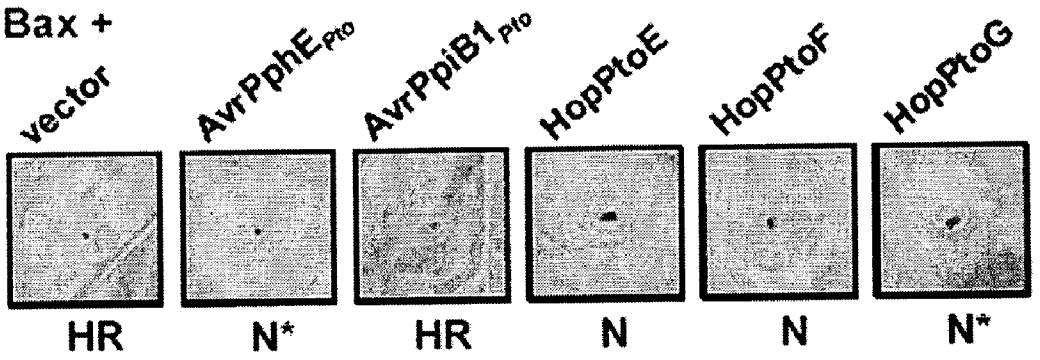


Figure 7A

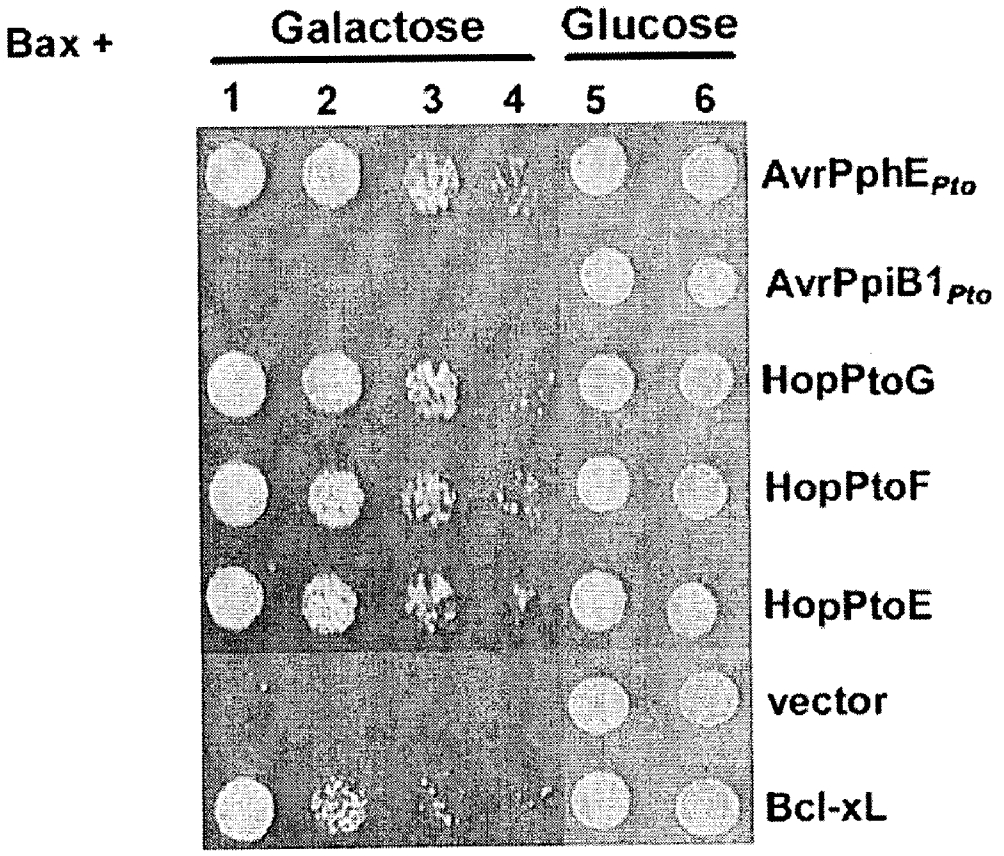


Figure 7B

PSEUDOMONAS AVR AND HOP PROTEINS, THEIR ENCODING NUCLEIC ACIDS, AND USE THEREOF

This application claims benefit of U.S. Provisional Patent Application Ser. Nos. 60/356,408, filed Feb. 12, 2002, and 60/380,185, filed May 10, 2002, each of which is hereby incorporated by reference in its entirety.

This work was supported by National Science Foundation Grant Nos. MCB-9982646 and IBN-0096348, National Science Foundation Plant Genome Research Program Cooperative Agreement DBI-0077622, and National Research Initiative Competitive Grants Program, U.S. Department of Agriculture, Grant No. 01-35319-10019. The U.S. Government may have certain rights in this invention.

FIELD OF THE INVENTION

The present invention relates to isolated DNA molecules corresponding to the open reading frames of *Pseudomonas syringae* pv. *tomato* DC3000, the isolated avirulence effector proteins and hrp-dependent outer proteins encoded thereby, as well as their various uses.

BACKGROUND OF THE INVENTION

The plant pathogenic bacterium *Pseudomonas syringae* is noted for its diverse and host-specific interactions with plants. A specific strain may be assigned to one of at least 40 pathovars based on its host range among different plant species and then further assigned to a race based on differential interactions among cultivars of the host. In host plants the bacteria typically grow to high population levels in leaf intercellular spaces and then produce necrotic lesions. In nonhost plants or in host plants with race-specific resistance, the bacteria elicit the hypersensitive response (HR), a rapid, defense-associated programmed death of plant cells in contact with the pathogen (Alfano & Collmer, *J. Bacteriol.* 179:5655–5662 (1997)). The ability to produce either of these reactions in plants appears to be directed by hrp (HR and pathogenicity) and hrc (HR and conserved) genes that encode a type III protein secretion pathway and by avr (avirulence) and hop (Hrp-dependent outer protein) genes that encode effector proteins injected into plant cells by the pathway (Alfano & Collmer, *J. Bacteriol.* 179:5655–5662 (1997)). These effectors may also betray the parasite to the HR-triggering R-gene surveillance system of potential hosts (hence the avr designation), and plant breeding for resistance based on such gene-for-gene (avr-R) interactions may produce complex combinations of races and differential cultivars (Keen, *Annu. Rev. Genet.* 24:447–463 (1990)). hrp/hrc genes are probably universal among necrosis-causing gram-negative plant pathogens, and they have been sequenced in *P. syringae* pv. syringae (Psy) 61, *Erwinia amylovora* Ea321, *Xanthomonas campestris* pv. *vesicatoria* (Xcv) 85-10, and *Ralstonia solanacearum* GMI1000 (Alfano & Collmer, *J. Bacteriol.* 179:5655–5662 (1997)). Based on their distinct gene arrangements and regulatory components, the hrp/hrc gene clusters of these four bacteria can be divided into two groups: I (*Pseudomonas* and *Erwinia*) and II (*Xanthomonas* and *Ralstonia*). The discrepancy between the distribution of these groups and the phylogeny of the bacteria provides some evidence that hrp/hrc gene clusters have been horizontally acquired and, therefore, may represent pathogenicity islands (Pais) (Alfano & Collmer, *J. Bacteriol.* 179:5655–5662 (1997)).

Virulence effector proteins delivered to or into host cells by type III secretion systems are key factors in the pathogenicity of many bacteria, including animal pathogens in the genera *Salmonella, Yersinia, Shigella*, and *Escherichia*, and plant pathogens in the genera *Pseudomonas, Erwinia, Xanthomonas, Ralstonia*, and *Pantoea* (Galán & Collmer, *Science* 284:1322–1328 (1999)). In plant pathogens, the type III secretion machinery is referred to as the hypersensitive response and pathogenicity (Hrp) system because secretion mutants typically lose their ability to elicit the defense-associated hypersensitive response in nonhost plants and to grow parasitically or be pathogenic in host plants (Alfano & Collmer, *J. Bacteriol.* 179:5655–5662 (1997)). These phenotypes demonstrate the importance of the Hrp system in bacterium-plant interactions, and global identification of effectors will be important for understanding the pathogenesis of bacteria that use type III secretion systems. Unfortunately, several factors have hindered searches for type III effector genes. These factors include: (i) effectors are often redundant with mutants having only subtle phenotypes; (ii) with few exceptions (see e.g., Miao & Miller, *Proc. Natl. Acad. Sci. USA* 97:7539–7544 (2000)) motifs that can identify proteins as substrates for type III secretion have not been recognized (Lloyd et al., *Mol. Microbiol.* 39:520–523) (2001); (iii) many effectors show no similarity to known proteins; and (iv) some pathogens have multiple type III secretion systems which deliver different sets of effectors (Cornelis & Van Gijsegem, *Annu. Rev. Microbiol.* 54:735–774 (2000)). Thus, a complete inventory of type III effector genes is lacking for any pathogen, although it seems that pathogens such as *Salmonella* may have many such genes (Worley et al., *Mol. Microbiol.* 36:749–761 (2000)).

Plant pathogen type III effector proteins are mostly designated Avr or Hop, depending on whether their primary phenotype involves plant reaction or secretion behavior. Many effectors were initially discovered through their ability to betray the pathogen to the host R (resistance) gene surveillance system, thereby rendering the pathogen avirulent on a test plant (Keen, *Annu. Rev. Genet.* 24:447–463 (1990)). Over 25 effector genes have been identified by Avr or Hop phenotypes in various *P. syringae* pathovars and races (Vivian & Arnold, *J. Plant Pathol.* 82:163–178 (2000); Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856–4861 (2000)). The encoded effectors seem to determine both basic pathogenicity and host range, but the number of such proteins produced by any single strain has not been systematically investigated. *P. s. tomato* DC3000 is known to carry at least three avr genes, avrPto (Ronald et al., *J. Bacteriol.* 174:1604–1611 (1992)), avrPtoB (Kim et al., *Cell* 109: 589–598 (2002)), and avrE (Lorang & Keen, *Mol. Plant-Microbe Interact.* 8:49–57 (1995)), with the latter being in the Hrp pathogenicity island along with five other candidate effector genes (Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856–486 (2000); Lorang & Keen, *Mol. Plant-Microbe Interact.* 8:49–57 (1995)).

The present invention is a further advance in the effort to identify, clone, and sequence Avr and Hop proteins or polypeptides from plant pathogens.

SUMMARY OF THE INVENTION

One aspect of the present invention relates to an isolated nucleic acid molecule that includes a nucleotide sequence which (i) encodes a protein or polypeptide having the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID

NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, or SEQ ID NO: 209; or (ii) hybridizes, under stringency conditions comprising a hybridization medium which includes 0.9×SSC at a temperature of 42° C., to a DNA molecule complementary to SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, OR SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, or SEQ ID NO: 208; or (iii) is complementary to the nucleic acid molecules of (i) and (ii). Expression vectors, host cells, and transgenic plants which include the DNA molecules of the present invention are also disclosed. Methods of making such host cells and transgenic plant are disclosed.

A further aspect of the present invention relates to isolated effector proteins or polypeptides encoded by the nucleic acid molecules of the present invention. Compositions which contain the proteins or polypeptides are also disclosed.

Yet another aspect of the present invention relates to methods of imparting disease resistance to a plant. According to one approach, this method is carried out by transforming a plant cell with a heterologous DNA molecule of the present invention and regenerating a transgenic plant from the transformed plant cell, wherein the transgenic plant expresses the heterologous DNA molecule under conditions effective to impart disease resistance. According to another approach, this method is carried out by treating a plant with a protein or polypeptide of the present invention under conditions effective to impart disease resistance to the treated plant.

A further aspect of the present invention relates to a method of causing eukaryotic cell death which includes: introducing into a eukaryotic cell a cytotoxic Pseudomonas protein of the present invention, said introducing being performed under conditions effective to cause cell death.

A still further aspect of the present invention relates to a method of treating a cancerous condition which includes introducing a cytotoxic *Pseudomonas* protein of the present invention into cancer cells of a patient under conditions effective to cause death of cancer cells, thereby treating the cancerous condition.

Yet another aspect of the present invention relates to a method of inhibiting programmed cell death which includes introducing into a eukaryotic cell susceptible to programmed cell death, a protein of the present invention that is a hypersensitive response suppressor, said introducing being performed under conditions effective to inhibit programmed cell death of the eukaryotic cell.

Yet another aspect of the present invention relates to a method of modifying a metabolic pathway in a cell which includes: introducing into a cell a protein or polypeptide of the present invention which interacts with a native cellular protein involved in a metabolic pathway, wherein the protein or polypeptide modifies the metabolic pathway through its interaction with the native cellular protein.

It is believed that bacteria have evolved effector proteins to make exquisite alterations in host metabolism. While plant disease resistance, suppression of programmed cell death, and cancer cell toxicity are important uses, as mentioned above, it is believed that these effector proteins can be used to modify or effect metabolic targets in eukaryotes, including both yeasts and higher order species, such as plants and animals. It is noteworthy that several of the effector proteins disclosed herein have homologs in other phytopathogenic bacteria. Thus, these proteins appear to represent a set of effectors that are conserved among *Pseudomonas, Erwinia, Xanthomonas*, and *Ralstonia* spp. By disrupting or augmenting the function of these effectors through, for example, transgenic expression thereof in a host plant, it is believed that use of these effectors may lead to widely applicable means for controlling diseases of plants.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. **1**A–C illustrate assays for Hrp system-dependent secretion in culture or translocation in planta of candidate effector proteins. *P. s. tomato* DC3000 and a Hrp secretion mutant derivative were used for tests of newly identified candidate effectors (**1**A–B). DC3000 or a DC3000 hrcC mutant (Yuan & He, *J. Bacteriol.* 178:6399–6402 (1996), which is hereby incorporated by reference in its entirety) carrying test ORFs (i.e., candidate effectors) fused to either the FLAG (F) or hemagglutinin (HA) epitopes were grown in Hrp-inducing media, and cultures were separated into cell (lanes 1–3) and supernatant (lanes 4 and 5) fractions and analyzed by SDS/PAGE and immunobloting. Lanes 1 and 4, wild-type DC3000; lanes 2 and 5, wild-type DC3000 (pTest-ORF); lanes 3 and 6, DC3000 hrcC mutant (pTestORF). As an additional control against leakage, pCPP2318 was included in all strains, which encodes the mature form of β-lactamase (β-lac). The presence of an epitope-tagged protein in the supernatant fraction of the wild type (lane 5), but absence in the hrcC secretion mutant (lane 6), indicated that the test ORF encoded a secreted product. In FIG. **1**C, an AvrRpt2 translocation assay was performed with DC3000 HopPtoG. Test strains were infiltrated into *A. thaliana* Col-0 (RPS2) and Col-0 rps2-201 (rps2) plants. Plant responses were scored 18 h after inoculation for hypersensitive response (HR) or no visible response (N).

FIGS. **2**A–C illustrate pHIR11-dependent HR is suppressed by HopPtoE, and a *P. s. tomato* DC3000 hopPtoE mutant exhibits an enhanced HR. FIG. **2**A is a schematic representation of the pHIR11-based suppression assay in *P. fluorescens* (Pf) 55. When DC3000 effectors are individually expressed in trans in Pf(pHIR11), they can potentially

suppress the HopPsyA-dependent HR. FIG. **2**B shows *N. tabacum* cv. *xanthi* leaves that were infiltrated with Pf(pHIR11) (left panel) or Pf(pHIR11, phopPtoE)(right panel). 'N' denotes no HR. FIG. **2**C shows quantitative differences in the ability of DC3000 wild-type (WT), hopPtoE mutant UNL139, and complemented mutant UNL139 (phopPtoE) to elicit the HR in *N. tabacum* cv. *xanthi* leaves. Different dilutions of bacterial cells/ml (1, 10^8 cells/ml; 2, 10^7 cells/ml; 3, 10^6 cells/ml; and 4, 10^5 cells/ml) were infiltrated into leaves, then leaves were photographed after 24 hr.

FIGS. **3**A–C illustrate that HR suppression is not due to blocking TTSS, and the TTSS is functional. FIG. **3**A is an image of an immunoblot showing that AvrPto is type III-secreted from DC3000 (WT), but not from a secretiondefective DC3000 hrcC mutant (hrcC). β-Lactamase (β-Lac) was used as a lysis control. C, cell pellet fractions; S, supernatant fractions. FIG. **3**B is an image showing that the HR elicited in *N. tabacum* cv. *xanthi* by DC3000 is inhibited when hopPtoE is expressed in trans. FIG. **3**C shows the results of *P. fluorescens*(pHIR11) mixing experiments in *N. tabacum* cv. *Xanthi*, demonstrating that HR suppression can occur when HopPtoE and HopPsyA are TTSS-delivered by different bacteria. pLN18 is a pHIR11 derivative that lacks hopPsyA, but encodes a functional TTSS. pCPP2089 (Huang et al., *Mol. Plant-Microbe Interact.* 4:469–476 (1991), which is hereby incorporated by reference in its entirety) is a pHIR11 derivative encoding a defective TTSS.

FIGS. **4**A–C identify *P. s. tomato* DC3000 effectors that suppress the HR on tobacco and *Arabidopsis*. FIG. **4**A lists DC3000 effectors that were tested in the pHIR11 assay. A 'y' indicates that the effector inhibited the HR, an 'n' indicates that it did not, and a 'y*' indicates that it partially suppressed the HR. Refer to the Materials and Methods for information regarding effector constructs. The nucleic acid and amino acid sequences of $AvrPphE_{Pto}$, $AvrPpiB1_{Pto}$, HopPtoB, HopPtoC, HopPtoD1, HopPtoD2, HopPtoF (previously designated $AvrPphF_{Pto}$ ORF2), HopPtoJ, and HopPtoK are disclosed in U.S. patent application Ser. No. 09/825,414 to Collmer et al., filed Apr. 2, 2002, which is hereby incorporated by reference in its entirety. The nucleic acid and amino acid sequence of AvrPto is reported at Genbank Accession L20425; Salmeron & Staskawicz, *Mol. Gen. Genet.* 239: 6–16 (1993), each of which is hereby incorporated by reference in its entirety. The nucleic acid and amino acid sequence of AvrPtoB is reported at Genbank Accession AY074795 and Kim et al., *Cell* 109:589–598 (2002), each of which is hereby incorporated by reference in its entirety. AvrPtoB was independently shown to suppress the programmed cell death elicited by AvrPto or by heterologously-expressed BAX in *Nicotiana benthamiana* (Abramovitch et al., *EMBO J.* 22:60–69 (2003), which is hereby incorporated by reference in its entirety). FIG. **4**B is an image of *N. tabacum* cv. *xanthi* leaves that were infiltrated with *P. fluorescens*(pHIR11) with different effector constructs (noted above each picture). Complete suppression of the HR is denoted with 'N'. FIG. **4**C is an image of the same strains (as illustrated in FIG. **4**B) infiltrated into *Arabidopsis* Ws-0, producing identical results.

FIGS. **5**A–B illustrate that the HR elicited by HopPsyA can be suppressed via *Agrobacterium* transient expression of effectors. In FIG. **5**A, *N. tabacum* cv. *xanthi* leaves were co-infiltrated with *A. tumefaciens* C58C1 carrying phopPsyA and another strain carrying each candidate suppressor. All of the suppressive effectors identified in the pHIR11 screen also suppressed the HR elicited by HopPsyA in this test. In FIG. **5**B, an immunoblot of plant tissues with different agroinfiltrations shows that each HA epitope-tagged effector was made in planta. The asterisks indicates a protein of the predicted size of the effector in that lane.

FIG. **6** is an image showing that *Pseudomonas syringae* pv. *tomato* DC3000 suppressor mutants display an enhanced ability to elicit the HR. *N. tabacum* cv. *xanthi* leaves were infiltrated with *P. syringae* strains that were 10-fold serially diluted from 10^8 cells/ml. The last dilution (10^6 cells/ml) that resulted in an HR is shown. In all cases, the mutants exhibit more HR at this dilution than the wild type, and this phenotype was complemented when the suppressors were provided in trans. The following strains were infiltrated: DC3000 wild type, WT; avrPphEPto mutant, UNL113; avrPpiB1Pto mutant, UNL114; avrPtoB mutant, UNL127; hopPtoF mutant, UNL109; hopPtoG mutant, UNL124. HR was scored for each sample: spotty HR (HR−); strong HR (HR+); or no HR.

FIGS. **7**A–B illustrate that *Pseudomonas syringae* pv. *tomato* DC3000 HR suppressors inhibit the PCD initiated by Bax in plants and yeast. In FIG. **7**A, *Agrobacterium* C58C1 strains carrying binary vectors that encode Bax or a specific effector were co-infiltrated into *N. benthamiana* leaves. Leaves were photographed after 7 days. N* indicates that the HR was nearly absent. Effector constructs were the same as in FIG. **4**. In FIG. **7**B, yeast strain EGY48 carrying plasmids that encoded for Bax (pJG4-5-Bax) and a specific effector were spotted on plates at 5-fold dilutions. Expression of Bax was induced by galactose, whereas effector expression was constitutive. Only AvrPpiB1 was unable to suppress Bax-induced killing. Bcl-xL (pGilda-Bcl-xL), an animal protein known to inhibit Bax-induced PCD, was used as a positive control.

DETAILED DESCRIPTION OF THE INVENTION

One aspect of the present invention relates to *Pseudomonas syringae* pv. *syringae* DC 3000 nucleic acid molecules which encode Avr or Hop effector proteins.

A first nucleic acid molecule encodes HopPtoI (ORF1) and has a nucleotide sequence according to SEQ ID NO: 1 as follows:

```
atgcttatcgggcacagcttgcatcacatgcgacccactgctgtggattctagcctaccaacttccgca

actagccagactatcagcaataccaaaagtcggctggatccgcatcgtgtccgtgaacttacattcatc

ggagtgggtagtagtgttgcctacctactcaatgagcttaatggtcgctttgccgatagcggggtaaca

acgccgtttttaggaaaagtcagtattgtaggcaaggacgactcttgggccgagaatgttcgtgggaaa

ggttatattaaccaccagactgaaattataagccaatgggaccaacaggttccaaaatatgatcctaac
```

-continued

tatgctgctcgtgccgaattttctgcgagtaaccgaagacagttgacgcgaacagtggagttaggcgca

gaacatttgaaagcacaggtaacaggcatttcgcgattggatgacggttgttttcgaataaatctggac

aatggccagattttgcaaagccgacagattgtactggggactggtgccggaccccataccagtatctgg

aacagcgttacatcacacactcaagcagaaaaacgactggacaacatcaaattgcatgagcagaaagcc

ttgcgtggcaaggtgctggacctggatgagtttatgcgagcgagtgatgcctctccccagacgtttgct

ggaaaaacggtggtgatacatggaccaaatgcaggcattgatgcagctgaacgtgccggggagcttggg

gcaaatgcggtttggtttacccgcagtacgaatccggtattgctggatggcaatcaactaaaattcgcg

ccagagctggccaaaagcgctatacataaagttgacaaattagatattcgcccaacaaaactagagaat

ggtttcgcattgcgactacattacagttcgctaggacaagactcacgggagccaaagaaggtgctagat

gcggactattatgtgtacgccatgggtcaagatattcataagccgggtagcgcagcggccatactaggc

agtcttcttgaccacctagaacctatatatgactacgatcaagtctatagcgaccagcctttcaagaca

gtaataggcttgcaaagtcgcggctccaatagcgataatggtttaattattgtcggggcggcagttgct

cagctggccactaatgttcagcatagctataaggaccacgcgttggatcgtatacttgaggaaatgacc

aggctccccgaaaagcaaacagaaaagctatcacaaatgctgttagaaggtgcgccatcagtacagatc

cagacatatctaaaaacctggcagttagatagcggtcaaccgccagataaacaggtactgcagaatcaa

gtagaaaactatctggcggcccgagactacttccagcggcaaaccaacgaacaaaagggcaacctggac

ggggttgccgcagaggtaaaaaatcaaaccttaaccgaggttgcatcggtcatcgtgtcaccacagtta

ggcacgatcaaggcctccgctgcagcattgtcgggacttatgccagcatatgtggctaacggcgaaaat

aactttaccaccgataatcgaactatgctccgtgccggcattgcagcaagatatccgaatataggtaac

gctgaagccagtgcatttatcgatgaagtagtaactttgcgtcaccttaatagtcagcgttttattgag

aaggtagcaggcgaaatgatggacaaaggagctcaaccactggtgtcgttacgccccccggtcctaggt

gtcccggcgtcggtcaggactgcttatgaggcttacttgcacgcgctgaattctggagcgcacgatggt

acgccgttaagtcagcgctggctgcccaaaaaatag

The HopPtoI protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 2 as follows:

MLIGHSLHHMRPTAVDSSLPTSATSQTISNTKSRLDPHRVRELTFIGVGSSVAYLLNELNGRFADSGVT

TPFLGKVSIVGKDDSWAENVRGKGYINHQTEIISQWDQQVPKYDPNYAARAEFSASNRRQLTRTVELGA

EHLKAQVTGISRLDDGCFRINLDNGQILQSRQIVLGTGAGPHTSIWNSVTSHTQAEKRLDNIKLHEQKA

LRGKVLDLDEFMRASDASPQTFAGKTVVIHGPNAGIDAAERAGELGANAVWFTRSTNPVLLDGNQLKFA

PELAKSAIHKVDKLDIRPTKLENGFALRLHYSSLGQDSREPKKVLDADYYVYAMGQDIHKPGSAAAILG

SLLDHLEPIYDYDQVYSDQPFKTVIGLQSRGSNSDNGLIIVGAAVAQLATNVQHSYKDHALDRILEEMT

RLPEKQTEKLSQMLLEGAPSVQIQTYLKTWQLDSGQPPDKQVLQNQVENYLAARDYFQRQTNEQKGNLD

GVAAEVKNQTLTEVASVIVSPQLGTIKASAAALSGLMPAYVANGENNFTTDNRTMLRAGIAARYPNIGN

AEASAFIDEVVTLRHLNSQRFIEKVAGEMMDKGAQPLVSLRPPVLGVPASVRTAYEAYLHALNSGAHDG

TPLSQRWLPKK

HopPtoI has been shown to be a protein that is secreted by DC3000.

A second nucleic acid molecule encodes HopPtoH (ORF2) and has a nucleotide sequence according to SEQ ID NO: 3 as follows:

```
atgatcactccgtctcgatatccaggcatctatatcgccccctcagtaacgaaccgacagcagctcac
acatttaaagaacaagcagaggaagcacttgaccatatcagcgccgcaccctctggcgataagctattg
cgaaaaatatccactcttgccagtcaaaaagatagaaaagtcacgctaaaagagattgaaataaataac
cagtgttataccgaagctgttctgagcagraggcaactggaaaagtacgaaccagaaaactttaacgag
aaccggcacattgcatcacagctatcacgaaaggggacctttaccaaaggtgaaggaagcaacgcgatt
attggctggtcaccagacaaagcaagcatacgcttaaatcagaatggctcaccgttacaccttggaatg
gataacgacgacaaaatcacgaccctagctcatgagctcgttcatgctcgacatgtgttaggtggcagc
tccttagcggatggcggagatcgctataatccacgtacgggatctggcaaagaggaacttagggccgtt
ggattagataagtaccgctattcacttacaaaaaaaccgtcagagaactccatccgagctgaacacggc
ctgcctctgcgcatgaagtacagggcacatcaatag
```

The HopPtoH protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 4 as follows:

```
MITPSRYPGIYIAPLSNEPTAAHTFKEQAEEALDHISAAPSGDKLLRKISTLASQKDRKVTLKEIEINN
QCYTEAVLSRRQLEKYEPENFNENRHIASQLSRKGTFTKGEGSNAIIGWSPDKASIRLNQNGSPLHLGM
DNDDKITTLAHELVHARHVLGGSSLADGGDRYNPRTGSGKEELRAVGLDKYRYSLTKKPSENSIRAEHG
LPLRMKYRAHQ
```

HopPtoH has been shown to be a protein that is secreted by DC3000. HopPtoH has significant homology (1e-114), as detected by BLAST search, to ORF3 from *Pseudomonas syringae* pv. *pisi* avrPpiC2 locus (Arnold et al., *Microbiology* 147:1171–1182 (2001); GenBank Accession No. CAC16702, each of which is hereby incorporated by reference in its entirety.

A third nucleic acid molecule encodes HopPtoE (ORF3) and has a nucleotide sequence according to SEQ ID NO: 5 as follows:

```
atgaatagagtttccggtagctcgtcagcgacttggcaggcagtcaacgatcttgtggagcaagtaagc
gagagaaccacgttgtctacgacaggttatcagacggcaatgggccgcttgaacaaaccggaaaaatca
gatgcggatgcgctgatgactatgaggagggcgcaacagtacacggatagcgcgaagcgaacttatatt
tcggaaacgctgatgaatctggcagatttgcagcaaaggaaaatctatcgcaccaacagcgggaacttg
cgtggcgcgattgagatgacgcctacgcaactcacagattgcgtacagaagtgccgcgaagaggggttc
tccaattgtgacatacaggcgctggaaatcggcttgcaccttcgacataagttaggaatctcagatttc
accatctacagcaaccgtaagttaagccataactatgtggtcatccaccccagcaatgcatttccgaaa
ggagcgattgtagactcttggacgggacagggcgtggtggagctggacttcaagacccgattgaaattc
aagcaccgggaagagaactacgcagtgaacgccaatatgcacgagtggatcgagagatacggccaagcg
catgtgattgactga
```

The HopPtoE protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 6 as follows:

MNRVSGSSSATWQAVNDLVEQVSERTTLSTTGYQTAMGRLNKPEKSDADALMTMRRAQQYTDSAKRTYI
SETLMNLADLQQRKIYRTNSGNLRGAIEMTPTQLTDCVQKCREEGFSNCDIQALEIGLHLRHKLGISDF
TIYSNRKLSHNYVVIHPSNAFPKGAIVDSWTGQGVVELDFKTRLKFKHREENYAVNANMHEWIERYGQA
HVID

HopPtoE has been shown to be a protein that is secreted by DC3000 as well as translocated in planta.

A fourth nucleic acid molecule encodes HopPtoG (ORF4) and has a nucleotide sequence according to SEQ ID NO: 7 as follows:

atgcaaataaagaacagtcatctctattcagcttcaagaatggtgcagaatacttttaatgcctcgcct
aagatggaagtaactaatgcaatagcaaaaaataatgaacctgctgcgctgagcgctacgcaaactgca
aagacacacgaaggcgattcaaaaggccaatccagcaataactctaaattgcccttccgcgccatgagg
tacgctgcataccttgcaggcagcgcctacctctacgataaaactgccaataatttttttctttctacc
acttctctgcatgatggcaaaggtggttttaccagcgatgccaggcttaacgatgcacaagataaagcg
cgaaagcgctaccaaaacaaccatagcagcactcttgaaaataaaaactcgcttttaagcccgcttagg
ctttgcggagagaatcagttcttaacgatgattgattatcgtgcagcaactaagatttacctctccgac
ctagttgacacggagcaagcgcacacatcaattctgaagaatattatgtgcctgaaaggtgagcttacc
aatgaagaggcaataaaaaaactcaacccggaaaaaacaccaaaagactatgaccttacaaatagcgaa
gcctatataagcaagaacaaatattctttgaccggcgttaaaaatgaggagacgggatctactggttat
acatctcgttctatcacaaagccatttgtggaaaaaggcctgaaacactttataaaagcgactcatggc
gaaaaagctctcacgcccaagcagtgtatggaaactcttgataacttacttcgaaaaagtatcacgctc
aacagtgattcccaattcgcagcaggccaggcacttttggttttcagacaggtctatgcgggtgaagac
gcttgggggggatgcggaacgggtcatattgaaaagccattataatcggggcactgtactccaagatgaa
gctgataaaatagaactaagtaggccgttctcagagcaagatttagcaaagaacatgtttaagaggaat
accagcattgcagggccagtgctctaccacgcatatatttatatacaagaaaaaatcttcaagctaccc
cccgacaaaatagaagatttgaaacataaatcaatggcagacttgaaaaacctgcctttgactcatgtt
aagcttagcaattccggtgtgggatttgaagacgcctcagggttaggagactcgtttacagctctcaac
gcgacgtcctgtgttaatcacgcaagaataatgagtggtgagcctcccttgtcaaaagatgatgttgtg
attctgataggttgcctcaacgccgtatacgacaattcgagcggaataaggcattctctccgcgaaatt
gcacgagggtgctttgtgggtgctggttttacggtccaggacggtgacgacttctacaaacagatctgc
aaaaacgcctctaagcagttttacaacggctaa

The HopPtoG protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 8 as follows:

MQIKNSHLYSASRMVQNTFNASPKMEVTNAIAKNNEPAALSATQTAKTHEGDSKGQSSNNSKLPFRAMR
YAAYLAGSAYLYDKTANNFFLSTTSLHDGKGGFTSDARLNDAQDKARKRYQNNHSSTLENKNSLLSPLR

-continued

LCGENQFLTMIDYRAATKIYLSDLVDTEQAHTSILKNIMCLKGELTNEEAIKKLNPEKTPKDYDLTNSE

AYISKNKYSLTGVKNEETGSTGYTSRSITKPFVEKGLKHFIKATHGEKALTPKQCMETLDNLLRKSITL

NSDSQFAAGQALLVFRQVYAGEDAWGDAERVILKSHYNRGTVLQDEADKIELSRPFSEQDLAKNMFKRN

TSIAGPVLYHAYIYIQEKIFKLPPDKIEDLKHKSMADLKNLPLTHVKLSNSGVGFEDASGLGDSFTALN

ATSCVNHARIMSGEPPLSKDDVVILIGCLNAVYDNSSGIRHSLREIARGCFVGAGFTVQDGDDFYKQIC

KNASKQFYNG

HopPtoG has been shown to be a protein that is secreted by DC3000 as well as translocated in planta by recombinant *Pseudomonas syringae* pv. *pisi*. Thus, HopPtoG appears to be a Hrp-injected effector protein. HopPtoG has significant homology, as detected by BLAST search (1e-137), to a hypothetical protein of *Ralstonia solanacearum* (see GenBank Accession No. NP_521884, which is hereby incorporated by reference in its entirety).

A fifth nucleic acid molecule encodes HopPtoS1 (ORF5) and has a nucleotide sequence according to SEQ ID NO: 9 as follows:

atgggtaatatttgtggtacttctggctccaatcatgtgtatagtccgcctattagccctcaacatgca

tctggttcgtccacaccagtgcccagtgcttctgggacgatgctttctctcagtcatgaacaaatatta

agccagaactatgctagcaatataaaggggaaatatcgcacgaacccccgaaaaggaccatctcctagg

ctttctgatacgctgatgaagcaggcgctgtcttcagtgatcacacaagagaaaaagcgacttaaaagt

caaccaaagtcaatagcccaagatattcagcctccaaacagcatgatcaaaaatgcacttgatgaaaaa

gacagccacccttttggtgattgcttttcagacgatgaatttcttgcgatccatctctatacgagttgt

ctttacagaccgatcaaccatcatctgcggtatgccccgaaaaatgatgtcgcgcctgttgtggaggca

atgaatagcggtttggccaaacttgctcaataccctgattatcaggtgtctggtcagctgcatagaggc

atcaagcaaaagatggatgatggtgaagttatgagtcgcttcaagccgggtaatacttatcgtgatgac

gcgttcatgageacatcgactagaatggatgttacagaagaatttacttccgatgtcacgttacatctg

cagtcctcatcagccgtcaatataggtccctttttcaaaaaacccatacgaggacgaagcgctcatcccg

cccctgacgcctttcaaagtaaccggtctgcacaagcaggacgataggtggcacgtccacttgaacgag

atcgcagagagctctgacgagtga

The HopPtoS1 protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 10 as follows:

MGNICGTSGSNHVYSPPISPQHASGSSTPVPSASGTMLSLSHEQILSQNYASNIKGKYRTNPRKGPSPR

LSDTLMKQALSSVITQEKKRLKSQPKSIAQDIQPPNSMIKNALDEKDSHPFGDCFSDDEFLAIHLYTSC

LYRPINHHLRYAPKNDVAPVVEAMNSGLAKLAQYPDYQVSGQLHRGIKQKMDDGEVMSRFKPGNTYRDD

AFMSTSTRMDVTEEFTSDVTLHLQSSSAVNIGPFSKNPYEDEALIPPLTPFKVTGLHKQDDRWHVHLNE

IAESSDE

HopPtoS1 has been shown to be a protein that is secreted by DC3000 as well as translocated in planta. HopPtoS1 has significant homology, as detected by BLAST search (1e-5), to a chicken ADP-ribosyltransferases (Tsuchiya, *J. Biol. Chem.* 269:27451–27457 (1994); GenBank Accession No. P55807, each of which is hereby incorporated by reference in its entirety), as well as significant homology to a type III-secreted ADP-ribosyltransferase from *P. aeruginosa* (Yahr et al., *Mol. Microbiol.* 22:991–1003 (1996), which is hereby incorporated by reference in its entirety). Further confirming its similarity to ADP-ribosyltransferases, HopPtoS1 has been determined to possess an ART domain (pfam1129).

A sixth nucleic acid molecule encodes ORF6 and has a nucleotide sequence according to SEQ ID NO: 11 as follows:

atgagcttatcgccgacgctgcaaaagctaactaatatattgggcccgac

aaaaaatgccaagcctgtcacagaggctatccagtggcaggaaggcatgg

-continued

atataacgctgcatgtcagcggcgacagccttaccttactagctaaaatc

atagaactgcgtacagaccctaaagacgacattttattgcgcaagctgct

tacccatacgtttccgggcctgcgtctgcgccgtggcgcgcttaccatca

accctgatggaagtgccctggttttctcttatgaacacgattttcacctt

ctggacaaagcccgttttgagagcctgctggccaactttgctgaaacggc

gcaggagcttcgagacacagcgacacattttcgttttaactga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 12 as follows:

MSLSPTLQKLTNILGPTKNAKPVTEAIQWQEGMDITLHVSGDSLTLLAKI

IELRTDPKDDILLRKLLTHTFPGLRLRRGALTINPDESALVFSYEHDFHL

LDKARFEsLLANFAETAQELRDTATHFRFN

Although the protein of SEQ ID NO: 12 possesses N-terminal Hop features and features shared by type III chaperones, this protein was shown not to be secreted by DC3000. Because ORF6 is located directly upstream of ORF17 (described infra), it is believed that the protein of SEQ ID NO: 12 is a type III chaperone for the protein encoded by ORF17.

A seventh nucleic acid molecule encodes ORF7 and has a nucleotide sequence according to SEQ ID NO: 13 as follows:

atgaaacaacgagcgacagtcatctgcaaacgtgacggccaggtgcttta

cgtacgcaaaccaaaatcccgctgggctttgccaggtggcaagattgaag

-continued

ccggggaaacgcctttccaggctgccgtgcgcgagctttgcgaagaaacc

ggtctggaaaatctcgatctgttgtacctggcggtgtacgagaaaggtga

ggtcacgcactacgtgttcaccactcaggttcctgcctacagcgagcctt

cgccccagaacgagatttctgcctgcaaatggcttgcgcccaaaaatctt

ggcgaccttaaggccagcagcgcgaccaaggctatcgtcaagtcgtatgg

ccgccaggctgaagacggtttactcagcgctaactag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 14 as follows:

MKQRATVICKRDGQVLYVRKPKSRWALPGGKIEAGETPFQAAVRELCEET

GLENLDLLYLAVYEKGEVTHYVFTTQVPAYSEPSPQNEISACKWLAPKNL

GDLKASSATKAIVKSYGRQAEDGLLSAN

This protein shares significant homology, as detected by BLAST analysis (3e-7), to MutT mutator of *Mesorhizobium loti* (Genbank Accession No. NP_104556, which is hereby incorporated by reference in its entirety). The protein of SEQ ID NO: 12 was shown not to be secreted by DC3000. Although this protein is not secreted, it may still be an effector protein, because AvrB similarly is not secreted in culture although it is translocated in planta (see van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999); Gopalan et al., *Plant Cell* 8:1095–1105 (1996), each of which is hereby incorporated by reference in its entirety).

An eighth nucleic acid molecule encodes ORF8 and has a nucleotide sequence according to SEQ ID NO: 15 as follows:

gtgctcgcttttgcatacgtcagcctgattagagagcagaaattggacatcaaaaaacgttggccttcc

agtgagcaggagttggtagaagtccgacggtttaacaaaaccctcgcccggctgccgcgtttccaggtt

cgcaatcgcctcacgccccgcttgattcdggcgctgctgcgggcggctcagattggtcgcgcgttgaaa

ccggtcaaacatgacctgcggattgaaacaaccatcgtcagcaccggtaacgtccctgtttcagtgcga

atcataaggcccaaaggcaaacccaaaggcgtggtgtttgatattcacggcggcggttgggtgatcggc

aacgcccagatgaacgatgacctcaatatcggtatcgttaacgcgtgcaacgtggcggtcgtgtccgtt

gattacagattggctttatcgacccccgtcgaagggctgatggatgactgcttttctgccgcatgctgg

ctgctgggtagcgactgtaaggagtttgccggcctgccggttattgtcgtcggtgagtccgcgggcggg

catcttgccgcagccactttgctcaaattgaaagccaggcccgacttgctcaagcgcgtagtcggcacg

gttctgtattacggcgtgtacgacctgaccgggacaaaaagcgttcgtaccgcaggcccggaaacgctg

gtgctcgacggcccgggcatggtcggcgcaatgcgcttgctcgccccggacagaaccgacgagaagcgc

cgcgagccgccgttatcgcccttgtatggcgacctcacggatctgccgcccgccctgatgtttgtcggc

gaactcgacccgctgctggacgacacgctggaaatggccgagcgatggaaaaactcggcagacgttgaa

atgcatcttctgcccgagtctccacatgggttcatccacttcccgactgccttggcgcgcaaggtactt

gcgcgcagccacgagtggataaacgcgaggatggaaggacggccttaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 16 as follows:

VLAFAYVSLIREQKLDIKKRWPSSEQELVEVRRFNKTLARLPRFQVRNRL
TPRLIQALLRAAQIGRALKPVKHDLRIETTIVSTGNVPVSVRIIRPKGKP
KGVVFDIHGGGWVIGNAQMNDDLNIGIVNACNVAVVSVDYRLALSTPVEG
LMDDCESAAcWLLGSDCKEFAGLPVIVVGESAGGHLAAATLLKLKARPDL
LKRVVGTVLYYGVYDLTGTKSVRTAGPETLVLDGPGMVGAMRLLAPDRTD
EKRREPPLSPLYGDLTDLPPALMFVGELDPLLDDTLEMAERWKNSADVEM
HLLPESPHGFIHFPTALARKVLARSHEWINARMEGRP

This protein shares significant homology, as detected by BLAST analysis (1e-12), to a putative esterase/lipase of *Mesorhizobium loti* (Genbank Accession No. NP_105776, which is hereby incorporated by reference in its entirety). The protein of SEQ ID NO: 16 was shown not to be secreted by DC3000. Although this protein is not secreted, it may still be an effector protein, because AvrB similarly is not secreted in culture although it is translocated in planta (see van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999); Gopalan et al., *Plant Cell* 8:1095–1105 (1996), each of which is hereby incorporated by reference in its entirety).

A ninth nucleic acid molecule encodes ORF9 and has a nucleotide sequence according to SEQ ID NO: 17 as follows:

atgcaaacctatataccctatccaaaaaaccctcccaccgttggtacagttctgctgacttcctatggc
tcattcgcccatgaaaacgagatacctaaatcttgtgctgccgacgctttaagagtaggcaaagagctc
gctgatggtttcgatggcgaggttcatcatctaggcgctctgatgctgatgatttccgactttccagca
gagccgctgctgaaagcatctgctgctaagaaaggttctttgctaggaattacttcgcttggctaccta
ttatcctatggatctactggtgaaaaagcgaagcgaatcatcgaagcaggttgtggtatttttctcgtc
agagtgagtggtgatattgaaaaccctaaagcaaaaattgaagtttatagctcttggtctgaataccag
aagttccttgaacccattttgaagacaggtgacttttatccagtgaaaacgtcgtcgttttccgaataa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 18 as follows:

MQTYIPYPKNPPTVGTVLLTSYGSFAHENETPKSCAADALRVGKELADGF
DGEVHHLGALMLMISDFPAEPLLKASAAKKGSLLGITSLGYLLSYGSTGE
KAKRIIEAGCGIFLVRVSGDIENPKAKIEVYSSWSEYQKFLEPILKTGDF
YPVKTSSFSE

This protein shares significant homology, as detected by BLAST analysis (3e-50), to ORF4 of *Pseudomonas serioboryae* (Genbank Accession No. BAA87063, which is hereby incorporated by reference in its entirety).

A tenth nucleic acid molecule encodes ORF10 and has a nucleotide sequence according to SEQ ID NO: 19 as follows:

atgatcaacctcacccacattgcgtcttcattggcgcgggcagcgctcagcgattcgacaaagccgaag
atggagcgcgcgataaacgtcgcgagccacatcgctggcaaagtcgcgttgcaggtcaccagctcatta
ctggagcagaaaggtctgcttaacgagcgtcagcagaaagggctctcgatgattctgaaggccttgagc
ggcaaggagccggtgaacaatgtcgagacgcacgaaggggggaggccgattcaatctggcgcgagccgcc
ttcgacgtggccagcgttgtctgggagcgcgacaagtcgatgcataacgtgatgagctttctgggcgtc
agcgacagcaagggcaagatgttgttctctctgggcaagaagctggcggatgcaatggccaagcctgag
cctggcaaggacaacagtgaggccacaaatgcgcgccatgcctatttctccagcaacttgaaactgaac

-continued

aagttgatgaacgacctcactgaccaggttttcaacaagattcgccagtcgaacggtgatcgcgtgcga

cgacccatgccagaaccattctggagaccttacggcgcccaacagcaagcgcgcccgcaaacgcctccc

ggcactcgcccacaagccaacagcgccccgccaccgccgccgaaagcagagccacgacctgcgtcgggc

cggcctgacggcgcccaacagcaggcgcgcccggaaacgccgcctcgtactcgaccgcaggccaatagc

actccgccaccgccgccgaaagcagagccacgacctgcgtcgggccggcctgacggcgcccagcagcaa

gcacgcccggaaacgccgccgcgcactcgcccgcaggcgaacagcacgccgccaccgccgcccaaggca

gagccacgacctgcgtccggccggcctgacggcgcccaacagcaagcacgcccggaaacgccacctcgc

actcgcccccaagcgaacagcgcgccgcctccgccgcccaaagcagagccacgacctgcgtccggccgg

cctgacggcacccaacagcaagcacgcccggaaacgccacctcgcactcgcccccaagcgaacagcgcg

ccgcctccgccgcccaaagcagaacccagcgcaggcggcgaacggccttcaacggcgcggcccaataac

acatcggctgctgacgcatctgccagggtgggcgattccgcacctgccaagccgcccgtcaagccgttg

tacgagcacttgggcctcactgacatgtcggtagacttatccgccgttaaaaaggcttacagagatgcc

gcgatgaagaaccaccctgataaaaaccgcggcaacgaggccgaggcggccgagcgcttcaaagtcatt

tcaaatgcgtacaagattttgtccgacccggagttgcgcaaagcatacgacaacggccgtatcaatgag

gctggtaatagggcatga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 20 as follows:

MINLTHIASSLARAALSDSTKPKMERAINVASHIAGKVALQVTSSLLEQKGLLNERQQKGLSMILKALS

GKEPVNNVETHEGGGRFNLAPAAFDVASVVWERDKSMHNVMSFLGVSDSKGKMLFSLGKKLADAMAKPE

PGKDNSEATNARHAYFSSNLKLNKLMNDLTDQVFNKIRQSNGDRVRRPMPEPFWRPYGAQQQARPQTPP

GTRPQANSAPPPPPKAEPRPASGRPDGAQQQARPETPPRTRPQANSTPPPPPKAEPRPASGRPDGAQQQ

ARPETPPRTRPQANSTPPPPPKAEPRPASGRPDGAQQQARPETPPRTRPQANSAPPPPPKAEPRPASGR

PDGTQQQARPETPPRTRPQANSAPPPPPKAEPSAGGERPSTARPNNTSAADASARVGDSAPAKPPVKPL

YEHLGLTDMSVDLSAVKKAYRDAAMKNHPDKNRGNEAEAAERFKVISNAYKILSDPELRKAYDNGRINE

AGNRA.

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted, and shares significant homology, as detected by BLAST analysis (2e-11), to DnaJ protein (Genbank Accession No. BAB17689, which is hereby incorporated by reference in its entirety).

An eleventh nucleic acid molecule encodes ORF11 and has a nucleotide sequence according to SEQ ID NO: 21 as follows:

atgaacattacgccgctcacgtcagccgcgggcaagggctcgtccgcacaaggcacagacaaaatttcc

attcccaactccacgcgcatgatcaatgccgcttcaatcaagtggttgaataaggtgcgtagcgccatc

agtgaccacatccgcaccagcatcgagaaagggaaactgttcgagctcgcctccttgggcagcaacatg

ttcggtgtcccggctctttcagcgcgcccctcgacgctccaacctgtgttggcgtttgaggctgacccc

aatcacgacctgaaccttgtcagggtctatatgcaggacagcgccggaaagctcactccctgggacccg

acgcccaacgcggtcacgacgacgtcgaatccatcagagcctgatgcgcagagcgatacggcttcgtca

tcattacctcggcggcctcccgcaggctcggtgctgagtttgctgggcattgcgctggatcacgcgcaa

-continued

cgccacagtcctcgcgcggacaggtctgccaagggacgacctggccgagaggagaggaacggggcaagg

ttcaatgccaagcaaacaaagccgacagaggctgaagcctacggtgatcatcagacacccaatcctgat

ttgcacaggcaaaaagagacagctcaacgcgttgctgaaagcatcaacagcatgcgagagcagcaaaat

ggaatgcaacgcgccgaagggcttctcagagccaaagaagcgttgcaagctcgggaagccgcgcgcaag

cagcttctggacgtgctcgaggccatccaggctggccgtgaagactccaccgacaagaagatcagcgcc

actgaaaagaacgccacgggcatcaactaccagtga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 22 as follows:

MNITPLTSAAGKGSSAQGTDKISIPNSTRMINAASIKWLNKVRSAISDHIRTSIEKGKLFELASLGSNM

FGVPALSARPSTLQPVLAFEADPNHDLNLVRVYMQDSAGKLTPWDPTPNAVTTTSNPSEPDAQSDTASS

SLPRRPPAGSVLSLLGIALDHAQRHSPRADRSAKGRPGREERNGARFNAKQTKPTEAEAYGDHQTPNPD

LHRQKETAQRVAESINSMREQQNGMQRAEGLLRAKEALQAREAARKQLLDVLEAIQAGREDSTDKKISA

TEKNATGINYQ

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted, and has significant homology, as detected by BLAST analysis (5e-7), to a HrpA-like protein (Genbank Accession No. AAB00126.1, which is hereby incorporated by reference in its entirety).

A twelfth nucleic acid molecule encodes ORF13 and has a nucleotide sequence according to SEQ ID NO: 23 as follows:

atgcgcacatccgttaatggtctgcttgagcacagcctgaagaccctgggctttgatacttcggcattg

caggccttgcgcgacgacggttatttactgtggcaaggcaaggataagcaagccagtcttctggttccc

tctactgacggcgacgcgcttttcgctatctgtaccttgagccgtgtcgatcccgagcacgacggacgt

ctgctggcgcttgcattgcacctgaacctgtctcctgtccacacgatgagcgcatgtatagcdcttgat

gtcgagcaaaacacgttgtgtcttcgctacacccatgaccttggcgggaacggggcagataccctgttg

cttgcgctcgaaaacgcccaagcgcttgctgaacagatcaagcaggtaatcgaaaactttaggcacgat

cagggacgccgatag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 24 as follows:

MRTSVNGLLEHSLKTLGFDTSALQALRDDGYLLWQGKDKQASLLVPSTDGDALEAICTLSRVDPEHDGR

LLALALHLNLSPVHTMSACIALDVEQNTLCLRYTHDLGGNGADTLLLALENAQALAEQIKQVIENFRHD

QGRR

Because ORF13 shares features common to type III chaperones and is located directly upstream of hopPtoS1 (ORF5), it is believed that the protein of SEQ ID NO: 24 is a type III chaperone for HopPtoS1.

A thirteenth nucleic acid molecule encodes ORF14 and has a nucleotide sequence according to SEQ ID NO: 25 as follows:

```
atgatcgcgttcgcaaccggactgctagaacacagcctgaaacggcttggatacgacgccgcagatttg

caatcccttcgggatgaagggtatttgctgtggcacgggaaaaacggtcacaccagcctgttggtgccc

gctgctggcgggatgcgctttttgtcatcagcaccctgagctacatcgatcctgaacaggacgggcgg

ctgctggcgcttgcgctgcatttgaacttgtcgccagcccacactctgggcgccagtatcgcgctggat

atcgagcaaaataccttgtgcctgcgttacacgcacgacctcactgggcacggcacagacaatttgtcc

cgcgcgcttgaaagcactcaggcacttgccgagcagatcaagcaggtcatcgaaacttccgcagtgaa

ttcggacgcccgccaatgcccgcccacacagcccgacggccagatgccctggcgctttag
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 26 as follows:

```
MIAFATGLLEHSLKRLGYDAADLQSLRDEGYLLWHGKNGHTSLLVPAAGGDALFVISTLSYIDPEQDGR

LLALALHLNLSPAHTLGASIALDIEQNTLCLRYTHDLTGHGTDNLSRALESTQALAEQIKQVIETFRSE

FGRPPMPAHTARRPDAVAL
```

ORF14 shares features common to type III chaperones and shares weak similarity with ORF8 of the DC3000 Conserved Effector Locus ("CEL") (U.S. patent application Ser. No. 09/825,414 to Collmer et al., filed Apr. 3, 2001, which is hereby incorporated by reference in its entirety), which is a candidate chaperone for the protein encoded by CEL ORF7. Thus, the protein of SEQ ID NO: 26 is likely a chaperone for the protein of SEQ ID NO: 28.

A fourteenth nucleic acid molecule encodes ORF15 and has a nucleotide sequence according to SEQ ID NO: 27 as follows:

```
gtgaaaaagtctggcgctggaactcaagcctatgcgttgttcgcctctgcgacgggaagctcgtcgaag

ggcgttctaagtaccattgccaggcacctgacgggatgttttgcacccaacaagactgcgcttcattca

gcaacagccgtttcgtatgagctattgccgggcaattattctgtcgccgccagtgtgcatggcttgtcg

gttgatcaccgccagccggcgctgacacgactgagtaacgtgctgttcaatcaggcactggcgctggac

ctggagcgttttgacgagggcgcgccagccgacgaaatgttcaggccttcactgaaacgcgaacgtgcc

catccccgattggccgactcactgggtggcgagcaactggctgtgcaaaccatggagaagggccttaaa

cggctggcagaggatcctgcgcagtcctttgcgcgatgccattcatttttttacccgatcagtagtgat

accacttcacctcaagcatcacttcattctgtggcgagctcatctggctga
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 28 as follows:

```
VKKSGAGTQAYALFASATGSSSKGVLSTIARHLTGCFAPNKTALHSATAVSYELLPGNYSVAASVHGLS

VDHRQPALTRLSNVLFNQALALDLERFDEGAPADEMFRPSLKREGAHPRLADSLGGEQLAVQTMEKGLK

RLAEDPAQSFARCHSFFYPISSDTTSPQASLHSVASSSG
```

The protein of SEQ ID NO: 28 does not share all of the N-terminal features associated with known Hops, however, it is 34% identical with the product of ORF 26, which does.

A fifteenth nucleic acid molecule encodes HopPtoT1 (ORF16) and has a nucleotide sequence according to SEQ ID NO: 29 as follows:

```
atgaaaacagtcagcaatcactcgatacccagtacaaatctcgtcgtggatgcgggaacggaaacttcg
gcgcagaaatcccagccggtttgcagcgaaatccagcgtaacagcaagatcgaaaaagcagtcatcgaa
cacattgccgaccacccggcagcgaaaatgacaataagcgcgctggttgacacgttgacagacgttttt
gtcagggctcatggggaggttaaggggtgggccgaaatcgtccaggcagtctctcgccctcatgacagt
aatcgacacggcagtggagtgctcagcccgcgctttgatgtaatggggagtgttggttggaatgcggca
gctatccgggccaccagtcgcgtcgggacgcttcgagagaaaggtacactgttcactaaccttatgctc
agtaacaactttaaacatttgcttaaacgagtggttaacgatccagccttgcagcaaaagctcgacggt
gggttagacctcaactatctgaaggcttgtgaaggcgatctttatgtcdtgtcagggtgggctgcacgg
gctagcgaaagtcgtgaacaaattggcaaagcccggtatgaaacggcatcaaatcttagccagacgctg
atcagtgcacgtgagttggcttttcatcgtcacaatccggttaatcatccgtctgcccaaacgaaagtg
ggcttcgataagggtttgcctgaggaatctgatctgcaggttctgagaggccatggcagcagtgtatgg
agtgtaaaaccgggcagcgatttcgcaaagcgtgctgaagtttctggaaagcctattatcgccggcccg
tccggtaccgcttcgcgcatggtcgctgttgcgcgttttctggcaccggcttgtttgaaaagcctgggt
attgagagtgagcagaacctgaaagagcttgtgcggtatgcctgctatgcctatttcggtcaggacagc
caccattcgatgcttgaagtgaatcttggtgtcgcttcccatggaatgccggaacaatgggacgacacg
ctttataacgagcctttcagtaattcaattaaaggtcgcgggtttggtatagacaatctcgcgcatagg
caagtcgtcaggcaggcggctcaaaagtcatga
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 30 as follows:

```
MKTVSNHSIPSTNLVVDAGTETSAQKSQPVCSEIQRNSKIEKAVIEHIADHPAAKMTISALVDTLTDVF
VRAHGFVKGWAEIVQAVSRPHDSNRHGSGVLSPRFDVMGSVGWNAAAIRATSRVGTLREKGTLFTNLML
SNNFKHLLKRVVNDPALQQKLDGGLDLNYLKACEGDLYVMSGWAARASESREQIGKARYETASNLSQTL
ISARELAFHRHNPVNHPSAQTKVGFDKGLPEESDLQVLRGHGSSVWSVKPGSDFAKRAEVSGKPIIAGP
SGTASRMVAVARFLAPAcLKSLGIESEQNLKELVRYACYAYEGQDSHHSMLEVNLGVASHGMPEQWDDT
LYNEPFSNSIKGRGFGIDNLAHRQVVRQAAQKS
```

HopPtoT1 has been shown to be translocated by DC3000 in planta.

A sixteenth nucleic acid molecule encodes ORF17 and has a nucleotide sequence according to SEQ ID NO: 31 as follows:

```
atgcggtttgatgctgcccgaggccagaagcccaaagcccctatggatgcaccgtcatcattacgtttg
cgagcgatagcaggtggcatgcccagtgaagaagcaggaacgactgcacctgctgacgtgaatcagcct
ccacctgctgatgttcgtccagaaatgggtgtaggtcctgtgagactcttcgttaaactgatggtagga
actctggcgctgtcgacaggagtccgttttgcaagatacccaggtgatttcgcgaaggatccgggaggc
agtgtatgggcagcaatcaatctgcagcatcgctcgagcgtcacacatcttgaacaaggcaataagacg
gttcttgagcgtttcggtgcacatattccaaaagacagtgcgtgtttcaaagctcgcgctgacgtcaca
```

-continued

cacgatgttccctcaggcgtggcagggcagtggaaccacaaaacccaacgggtaaaactgaaccctaac

attcatttcgagagccatccggcacaggtcgccggacatgagttcatacactgttacacgcatcctgag

tttgtcgaacgccatataaaacatccgcactggaaagccctgaacgaagggttgacgactcgtttgaca

gagaaactgccagaccctaagcgtctcttgcccattcccttggcaaaggatccctatcatggtttcaag

ctgtccaccggggactcctggccggatgcggccaggcgaatcgaagacgaagttggcgaagatgtgttg

ttgaaagcgttctttggcggcgatgaccaggctattagtgaagtagctaaagccgctgctcagatctac

cccaagattgcctcacgtattaccgagagggagttgtatcaagcgggcagcatgcgtggaggacaacag

ctggccgagtgttacgtaggtgctttgctcaaaaacggtcagaaactgcctgacagttttacgaattat

ctgctacctgtatttagctattcagatataagccctggtcacgcgaaaaaaatacaggcgcaagcggaa

aaaagtcaaaagcggatgggaattgtgttcgatacagcgtttttttcacctgacctgaagacccagaga

ctggcacttggcatgctacgggaggacctgctgatgcactggaaaaaagttattccggatagaaagtaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 32 as follows:

MRFDAARGQKPKAPMDAPSSLRLRAIAGGMPSEEAGTTAPADVNQPPPADVRPEMGVGPVRLFVKLMVG

TLALSTGVRFARYPGDFAKDPGGSVWAAINLQHRSSVTHLEQGNKTVLERFGAHIPKDSACFKARADVT

HDVPSGVAGQWNHKTQRVKLNPNIHFESHPAQVAGHEFIHCYTHPEFVERHIKHPHWKALNEGLTTRLT

EKLPDPKRLLPIPLAKDPYHGFKLSTGDSWPDAARRIEDEVGEDVLLKAFFGGDDQAISEVAKAAAQIY

PKIASRITERELYQAGSMRGGQQLAECYVGALLKNGQKLPDSFTNYLLPVFSYSDISPGHAKKIQAQAE

KSQKRMGIVFDTAFFSPDLKTQRLALGMLREDLLMHWKKVIPDRK

While the protein of SEQ ID NO: 32 does not possess several N-terminal features associated with known Hops, ORF17 is preceded by a good candidate chaperone protein, encoded by ORF6. Furthermore, the protein of SEQ ID NO: 32 has been shown to be translocated by DC3000 in planta.

A seventeenth nucleic acid molecule encodes ORF18 and has a nucleotide sequence according to SEQ ID NO: 33 as follows:

atgaacaggcttcacaagaccagtctgctggcggctatattgaccgcatccccctgcattatggcagct

aacgctcatgctatgagttgtcctgtcccgcaaagcgtgaagtacgttaatggtatctatatcgcgccg

gaaacgtttgctggttgggaggggaactgggtttctcaaccacacaagaaacactccattaaagagttt

tccactgctttatatctttcagtggataaaagtcagaagggaggaacattgactaactgtagttattca

ctaagcggagataatggcgtaatagatcttgagtatcgaaaatcaggaaatgagaatagactaaagaca

cttatcgtttccattgaaggtcagcacaattggattaaagagcgtggcgcggttggaattcaaggatat

gaatgtacaaagtcagcatctgagtgtcagttcgttccgctgcggctaaacgaggactga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 34 as follows:

MNRLHKTSLLAAILTASPCIMAANAHAMSCPVPQSVKYVNGIYIAPETFA
GWEGNWVSQPHKKHSIKEFSTALYLSVDKSQKGGTLTNCSYSLSGDNGVI
DLEYRKSGNENRLKTLIVSIEGQHNWIKERGAVGIQGYECTKSASECQFV
PLRLNED

This protein has significant homology, as detected by BLAST analysis (1e-6), to a putative *Yersinia pestis* exported protein (Genbank Accession No. NP_406993, which is hereby incorporated by reference in its entirety).

An eighteenth nucleic acid molecule encodes ORF19 and has a nucleotide sequence according to SEQ ID NO: 35 as follows:

atgcatcgtcctatcaccgcaggccataccacctcacgtctcatcctagatcagtcaaaacaaatatca
cgtaccccatcggaaagtagcgcgcaatcagcgctttctcagcaagcaagcatgagcagcccagttttg
gagcggtcgaaaagtgcgccagctttattgactgcggcacagcgcacgatgcttgcacaagtgggagcc
tgtaacgctcatctgacctcagatgaaaacatggccatcaacgaactgacatcacacaagccccttta
cctaaggatacgtggtttttcactgatcctaacaaggacccagatgatgtcgtgacctacaccttgggc
aagcaattgcaggctgagggctttgtgcacatcacggatgtagtggcgacactgggtgatgctgaagtt
cgctctcaacgtgccgagatggccaaaggcgtgttcaacaagcttgagttgcatgacgtgcatgtgtcg
cgtggtcgggattacgcaatgaattcgcttcagtcgaaggaacatgccaaatttttactggaaggtcat
gctttaagggctggacctggtgaaatacaccgcgacagcttgcaggacatgagcaggcgcctggcccgt
gcgccacatggagtcggtattgtcgtaattgcaggcatgagtgatatcaatgcgctcatcactacctgc
ccggatatggtgcgcgaacgggttgatgacatcaccatcatgggcggcgtcgagcctttaaaggacgca
gatggttttgtacagcctgatgcacgcgcttacaacaatgcgaccgacatggacgctgcgcgcagtctt
tatcggaaagcgcaggagcttggcattccacttcgtatagtgacaaaggaggcggcctataaaacggcg
gtttcgccttcattttacgaagggatagcggggagcggacatccagtaggccactacctgagagacgtt
cagaagagtgcgttgaaaggcctctgggaaggtattcaagctggattgcttcccgggttggatgactca
tggttctttcggacgttcatgccgaatgcacagattgaagcagcacaactggataaaaataaagagagt
tcgtttgaagatatctggcctaaggtgacgaagctaaacctgtatgatcctctgacattactggcctca
gtgccaggggcggcaaaactgctatttaaaccaaaagctatacacacagaaggatttggtgttgtagag
caagtaggtccagatgatgtgacgcatccagagaaagcaaagttattgatgtccgctttagccaaatct
gcgcttgtccagtcgacggtagccccagattga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 36 as follows:

MHRPITAGHTTSRLILDQSKQISRTPSESSAQSALSQQASMSSPVLERSKSAPALLTAAQRTMLAQVGA
CNAHLTSDENMAINELRSHKPLLPKDTWFFTDPNKDPDDVVTYTLGKQLQAEGFVHITDVVATLGDAEV
RSQRAEMAKGVFNKLELHDVHVSRGRDYAMNSLQSKEHAKFLLEGHALRAGPGEIHRDSLQDMSRRLAR
APHGVGIVVIAGMSDINALITTCPDMVRERVDDITIMGGVEPLKDADGFVQPDARAYNNATDMDAARSL
YRKAQELGIPLRIVTKEAAYKTAVSPSFYEGIAGSGHPVGHYLRDVQKSALKGLWEGIQAGLLPGLDDS
WFFRTFMPNAQIEAAQLDKNKESSFEDIWPKVTKLNLYDPLTLLASVPGAAKLLFKPKAIHTEGFGVVE
QVGPDDVTHPEKAKLLMSALAKSALVQSTVAPD

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted, and has significant homology, as detected by BLAST analysis (2e-92), to a putative protein of *Ralstonia solacearum* (Genbank Accession No. NP_518366, which is hereby incorporated by reference in its entirety). Furthermore, the protein of SEQ ID NO: 36 has been shown to be translocated by DC3000 in planta.

A nineteenth nucleic acid molecule encodes ORF20 and has a nucleotide sequence according to SEQ ID NO: 37 as follows:

```
atgcgttccagggttataactacatcgctggtagtcattatgctctcatgtgcatcagccgctccagct
tgcttctccgcagacatgactcccagcgtgtcgaacgagagcacgtcggaggcggattttcagcaatgg
ctggctactttccgcagcaatgcaactactaagggcatcgacacagccacactcgatcttgctttccaa
aacatcacgcttgacccgactgtgcaccagttggatatggcgcaaccagagttcacgacggccatctgg
gattatttgtctgaacgtctgactccgaagaatatccagcaagggcaggagcttctgcaaaaagagcca
gttctgaacgaggtagagcgtcactacggtgtggatgcgaagattatcgcggccatctggtgtattgaa
agcggctacggtaaggatattggtagtcgcgatgtgattcgttccttggccacgcttgcttacaagggc
cggcggatggattacggggctacacagttgatggccgcccttcatatcgtgcaaaacaaagacatcgcc
cgtgcgcaattgattggctcgtgggctggcgcgatggggcagacgcaattcatcccgacgacctatctc
gactatgcagttgattttaaccacgacaatcggcgcgacgtttggagttcccgggccgatgcgctggcc
tccactgcctcttatttacaacgcagcgcttggaactcgcgcgtctcttggggacaggaggtgcagttg
cccgagaatttcgattacgctcaggctgacatgtcgatcaagaagcccgttgccgaatggcaacggctc
ggggtgatgggaacgaagcaagcgattccgggcgagctcgcacaggagcaagcatcggtcctgctgccc
gcaggttatcgcgggccagcatttatggtcctaagtaatttccgtagcatcctgcgctataacaactcc
actgcctatgcgctaacgatcgggctactagccgacagttatgctggcgggaccggcgtgtctcacccg
tggccaactgataatcctcccttgggcagcattgcgcaggtaaccgatttgcagaaactgctgactgct
aagggctactccctgggtgctgctgacggtgttataggggcgatgacccgggcggccatccgggcttac
cagaaggatcagcatttgccacccgacggttacgccagcactgtactactggagagcctgcgccgatag
```

```
gtgaaaatcaatctccccgcgctcagaacaacgtcttcacgcgtgcagat
ctgcttgaccgcagtcctgctgtgcacaccgctgctgttttccgcgcatg
cccaggcagccggcacggcttctgaacaagccaatgtggaagtgatgatt
cgtcagctcaacgcgctcgaggccgtcgcccagcgcagtgtcgatcttcc
acaagacccggcccaacgctatcacctggactatccccggttggtcagcg
acatcgcgcgcatccgccagggcttgcaagactacctgtcgccgtcccgc
gcacagccccgcgaccccgtggagctatcaggccattacaacgtcagcgg
tgatcacacgccatga
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 38 as follows:

```
VKINLPALRTTSSRVQICLTAVLLCTPLLFSAHAQAAGTASEQANVEVMI
RQLNALEAVAQRSVDLPQDPAQRYHLDYPRLVSDIARIRQGLQDYLSPSR
AQPRDPVELSGHYNVSGDHTP
```

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A twentieth nucleic acid molecule encodes ORF21 and has a nucleotide sequence according to SEQ ID NO: 39 as follows:

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 40 as follows:

```
MRSRVITTSLVVIMLSCASAAPACFSADMTPSVSNESTSEADFQQWLATF
RSNATTKGIDTATLDLAFQNITLDPTVHQLDMAQPEFTTAIWDYLSERLT
PKNIQQGQELLQKEPVLNEVERHYGVDAKIIAAIWCIESGYGKDIGSRDV
IRSLATLAYKGRRMDYGATQLMAALHIVQNKDIARAQLIGSWAGAMGQTQ
FIPTTYLDYAVDFNHDNRRDVWSSRADALASTASYLQRSAWNSRVSWGQE
VQLPENFDYAQADMSIKKPVAEWQRLGVMGTKQAIPGELAQEQASVLLPA
GYRGPAFMVLSNFRSILRYNNSTAYALTIGLLADSYAGGTGVSHPWPTDN
PPLGSIAQVTDLQKLLTAKGYSLGAADGVIGAMTRAAIRAYQKDQHLPPD
GYASTVLLESLRR
```

This protein has significant homology, as detected by BLAST analysis (1e-106), to a putative transglycolase from *Pseudomonas aeruginosa* and *Ralstonia solanacearum* (respectively, Genbank Accession Nos. NP_252681 and NP_522801, each of which is hereby incorporated by reference in its entirety).

A twenty-first nucleic acid molecule encodes ORF22 and has a nucleotide sequence according to SEQ ID NO: 41 as follows:

```
atgcttgctcctgacggcgtagaaatcgatatcgtgctatcaggtatatgcggaactgatctggcggta
ttgtcgggccgtgaaggtggagaggtgggcattatacgcgggcacgaagcagttggcattattatcgat
gtaggtaaggatgtagtacacctacaaaaagggatgcgggtggtggttgatcccaacgaatactgtggc
gtttgcgaaccttgccgtcttgctaaaacgcacctatgcaatgggggggtgaacgctgggttggatatc
gcaggtgtcaacaaacatggaacttttgccgagcgcttcgttactcgtgagcgttttgtgtatcaattg
ccagacgatatgagctgggcagctggtgtgttggttgagcctgttgcctgcattctgaataatatagac
caggcgttcattcgagcgggagagcgtgtgttgatcctagggtctggccctatgagtctgattgcgcag
atcgttctgcgctcaatgggagttgacacgctcgccactgatcgaaacacacatcgcatacagttcggc
cgctcacaaagtcttgatgttatacatgccgatgatcttgagttgcagatgcagcaccaagaaaagttt
gatgttgttatcgatactgtcggtaatcagatcgatacagcttcacgctacatcggtcgcggtgggaga
attgtacttttggatttgatagtgactatcactacatgctgcctgtaaagtacttcctggttaacgct
atcagtattatttctgctggagaatacaatcagcactttcctagagcaattcgtcttgtgcaaaaactt
cctgagctagggcggctggtaacgcatcgctacgtactagaaaatcactcggaggttttcgatgcactt
ctgaacgatgcttccgcccccaatataaaaagcgtattcacaccaaatctcgcttatctttaa
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 42 as follows:

```
MLAPDGVEIDIVLSGICGTDLAVLSGREGGEVGIIRGHEAVGIIIDVGKD
VVHLQKGMRVVVDPNEYCGVCEPCRLAKTHLCNGGVNAGLDIAGVNKHGT
FAERFVTRERFVYQLPDDMSWAAGVLVEPVACILNNIDQAFIRAGERVLI
LGSGPMSLIAQIVLRSMGVDTLATDRNTHRIQFGRSQSLDVIHADDLELQ
MQHQEKFDVVIDTVGNQIDTASRYIGRGGRIVLFGFDSDYHYMLPVKYFL
VNAISIISAGEYNQHFPRAIRLVQKLPELGRLVTHRYVLENHSEVFDALL
NDASAPNIKSVFTPNLAYL
```

This protein has significant homology, as detected by BLAST analysis (2e-18), to a putative sorbitol dehydrogenase (Genbank Accession No. NP_389115, which is hereby incorporated by reference in its entirety).

A twenty-second nucleic acid molecule encodes ORF23 and has a nucleotide sequence according to SEQ ID NO: 43 as follows:

```
atgaaagttactgtattcagtcagatatcaattgatggcaagttgacgatgggcaaaggcgcatccagc
aagccgttgtttcagaactttgatgatgatgacatgcgttttattcataagttccgcggcgaagtcgac
gcaatcatggtagggcgcaatacaattgttactgacgatccacaattgaccaatcgctatgagtcgggt
cgtaacccaatacgtatcattcccaccacctccttagatctgcctacttccgccagtattttcaaatca
ccagagaaaactattatcgcaactagcgaacaggctcgtgatcatgaaatggtcaaacatatccgtgct
tgtggaaaggaggtgctctttgccggtgcaaagcatgtcgactttacacgacttttccctatgctggag
gcgcgcggaataaaccacatcatggttgagggcggtggccacctgaactggcaggtattcaatctcgat
ctggtagatgaaattatactcatgcaggtgcctatcatcataggtggtgcggcaactgcaacgcttgct
gacggggtggggtatcgggatatcaacatggccaattcgtttacgctgcatgctttagaagcacgcccc
cattacaatctcatgcacttcaagcgcgaatcgaacaatcggagcccgtactga
```

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 44 as follows:

MKVTVFSQISIDGKLTMGKGASSKPLFQNFDDDDMRFIHKFRGEVDAIMV
GRNTIVTDDPQLTNRYESGRNPIRIIPTTSLDLPTSASIFKSPEKTIIAT
SEQARDHEMVKHIRACGKEVLFAGAKHVDFTRLFPMLEARGINHIMVEGG
GHLNWQVFNLDLVDEIILMQVPIIIGGAATATLADGVGYRDINMANSFTL
HALEARPHYNLMHFKRESNNRSPY

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted, and has significant homology, as detected by BLAST analysis (8e-38), to a riboflavin specific deaminase (Genbank Accession No. NP_213307, which is hereby incorporated by reference in its entirety).

A twenty-third nucleic acid molecule encodes ORF24 and has a nucleotide sequence according to SEQ ID NO: 45 as follows:

atggagcaggaaaagagttcctgtttgcgctacggcgtgacccttaatga
aaaagatctgtcacgttttttgggaactacacagcactacatgtggagca
cgattaaaaatgagtacgcgctcactgaatccatcgaccacttgatggca
cagcatcaacagcaattaatgcgctcaatcagttttgaattgtttcaatc
catgcctggcgtggaggcgcttctcaatttactggagcataccggagtgc
cctgtgccgtagcctcttcgtctccacgtaatttggtcgagcttatattg
aagaaaacgaaattgcgtcgatttttcaaagaggttatttgtggtactga
tgttaaagagagtaaaccgaatccggagatttttcttacggcggccaagg
gacttggagtgtcacctcgtgcatgtctggttattgaagactcccatcac
ggtgttaccgctgcgaaggccgcccatatgttttgtataggtttgcgtca
ttccagctcatttcagcaggatctgagcgctgctgatctgatcgccaata
atcattatgacatcaagcaatggtttgcagaaaaatag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 46 as follows:

MEQEKSSCLRYGVTLNEKDLSRFLGTTQHYMWSTIKNEYALTESIDHLMA
QHQQQLMRSISFELFQSMPGVEALLNLLEHTGVPCAVASSSPRNLVELIL
KKTKLRRFFKEVICGTDVKESKPNPEIFLTAAKGLGVSPRACLVIEDSHH
GVTAAKAAHMFCIGLRHSSSFQQDLSAADLIANNHYDIKQWFAEK

This protein has significant homology, as detected by BLAST analysis (5e-32), to a putative phosphatase from Clostridium (Genbank Accession No. NP_347269, which is hereby incorporated by reference in its entirety).

A twenty-fourth nucleic acid molecule encodes ORF25 and has a nucleotide sequence according to SEQ ID NO: 47 as follows:

atgaatgcgttcgcaaccggtcagcttgaatacagcctgaaaaagctggg
atacgatgccgccgctttgcaggccctgcgcgaagaagggtacttgctgt
ggaaagggaaaaacgaccagaccagcttgctggtgccctcggccgatctg
gatgcacttttcgttatcaacacgttgagctacatcgaccccgagcatga
cgcacgtctgctggcgcttgcattgcaccttaacctgtcccctgtccata
cgatgagcgcctgcatagccctcgatgtcgagcaaaacacgttatgcctg
cgctacacccatgaccttggcgggagcggggctgataccctgttgcttgc
gctcgaaaacgcccaggcgctggccgaacaggtcaggcaggtgatcgaaa
ccttcaggcgtgaccaagggcgtccgtccgggcaaacgtctttgtcccgg
caatccagtgctctgatgcgataa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 48 as follows:

MNAFATGQLEYSLKKLGYDAAALQALREEGYLLWKGKNDQTSLLVPSADL
DALFVINTLSYTDPEHDGRLLALALHLNLSPVHTMSACIALDVEQNTLCL
RYTHDLGGSGADTLLLALENAQALAEQVRQVIETFRRDQGRPSGQTSLSR
QSSALMR

This protein shares features common to type III chaperones and is a putative chaperone for the product of ORF26 (described below).

A twenty-fifth nucleic acid molecule encodes ORF26 and has a nucleotide sequence according to SEQ ID NO: 49 as follows:

atgaaaatatccggctccacatcgcctgcacacacttcaacgaattccgc
gcagaagtcctcttcaaaagggctgctgagtggtttggccaagcatttca
aggggatgctcgtttctggcaacacttctggtcattcggcgctcgggcat
tacgcgtcatccagcagcggctccaaaggcaaggcaccggtacgggacga
ttacagcaacggaccgcaaacacgccttaacaacacacctctgaaacgag
cactggcccgagagcttgatcgctttggctacggttcatcggcgaccgag
tcttttgaccgctcattgcagcgtaaggataaaaatccagagcttgggaa
ggtctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 50 as follows:

MKISGSTSPAHTSTNSAQKSSSKGLLSGLAKHFKGMLVSGNTSGHSALGH
YASSSSGSKGKAPVRDDYSNGPQTRLNNTPLKRALARELDRFGYGSSATE
SFDRSLQRKDKNPELGKV

The protein of SEQ ID NO: 50 has been shown to be translocated by DC3000 in planta.

A twenty-sixth nucleic acid molecule encodes ORF27 and has a nucleotide sequence according to SEQ ID NO: 51 as follows:

atgaaaaaatgtattgctctgctccttactctggtcgtctgcgaaggtgcattggcaggdacggcacgt

gatgaacagaacatcacgtcttacatcgacagtcacggcaccgaacagatcgcgttgcttgagaagctg

gtcaacatcaacagcgggacagacaacgttgagggtgtcgtcaaggtcggtaacctgatcaagccggag

ctggaggcgttgggtttcgagaccgcctggcacgacctgccctcggcaatgaaccatgccggcagcctt

gtcgctgtgcatgacggcagcaagtctgcaaaacgtattctgctgataggccatctggatacggtcttt

cctcaaacaagccgctttcagacgttcgcttacctggacggcggcaaaaaagccaagggccccggcgtc

attgatgacaaaggcggcgtggtcacgatgctttatgcattgcaggcgctcaagcacagcggcgcgctg

gaaaagatgaacatctcggtagtcttgataggcgatgaagagctggcggccaaaccgaccgagatttcc

agagagtggctgatcgccgaagccaaaagaagcgacattgcgctgggcttcgaattcgccttgtcgccc

aatcaactgatcaccgagcgaagagggctgagcgaatggtttttgaccagcaccggcatcgacaaacat

tcagcgacgatctttcagcctgagaccggttttggtgcgatgtacgagtcggcccgagtgcttgacgag

attcgtcagaaactgtcgaacgagcagggcctgaccatcaatccgggactcattctgggcggctcaacg

gctgtggaagatagcgccagtgggcaaggcacggcttctggaagaaagacaacagttgcccggatcacg

tcggtgcatggtgatttgcgcttcagcagtgaagaccagagggcctctgcggaaacccgaatgaaggac

atagccagtcacccgctgccgcagaccaacagcgacctgaaaataaaagccatcatgccggtcatggcg

gatcgcgaaagcaatcgccaactactggcagcctacagtcaggtcagccaggatctcgacggacctgct

ttggagtcggcgccttcagcagaacgaggcggcgcagatatttcctatgtgaacaagtatgtgactgcg

agcctggacggtcttggtgcgtgggggcaggtgcgcacagtgaaaatgaaaccatcgagttgggctcc

ttgcccgtggtgacgaaacgggcggctattttcctgagccgctatggtaaccagtga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 52 as follows:

MKKCIALLLTLVVCEGALAGTARDEQNITSYIDSHGTEQIALLEKLVNINSGTDNVEGVVKVGNLIKPE

LEALGFETAWHDLPSAMNHAGSLVAVHDGSKSAKRILLIGHLDTVFPQTSRFQTFAYLDGGKKAKGPGV

IDDKGGVVTMLYALQALKHSGALEKMNISVVLIGDEELAAKPTEISREWLIAEAKRSDIALGFEFALSP

NQLITERRGLSEWFLTSTGIDKHSATIFQPETGFGAMYESARVLDEIRQKLSNEQGLTINPGLILGGST

AVEDSASGQGTASGRKTTVARITSVHGDLRFSSEDQRASAETRMKDIASHPLPQTNSDLKIKAIMPVMA

DRESNRQLLAAYSQVSQDLDGPALESAPSAERGGADISYVNKYVTASLDGLGAWGAGAHSENETTELGS

LPVVTKPAAIFLSRYGNQ

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted, and has significant homology, as detected by BLAST analysis, to a carboxypeptidase from Bacillus (4e-29) and a hydrolase from Ralstonia (5e-22) (Genbank Accession Nos. NP_241218 and NP_521834, respectively, each of which is hereby incorporated by reference in its entirety).

A twenty-seventh nucleic acid molecule encodes ORF28 and has a nucleotide sequence according to SEQ ID NO: 53 as follows:

atgaaccctataacacacagctttagtcatcttgggttttcaaacgctcaaagtacgtcagcgctggcg

cccggcggtaataaagtgccgaactttgtttcgcgagggcgaggcaaaggagtcccgcttgagcatttc

aacaccgctgatgagtatcgtttggcacgccagcagggcggcgtgctgaaatcaatagacggcagagag

ttcatgctactgctgcagaagtacacggccgccgaaacaagcgacgaagaatttgcggatttgagggcc

-continued

gccataccgcgctattccattgacctggccgagccgggtcaaactaaagtgctttatcgggggatatcg

ctgccggagaagactgcggcgcgattactgaatatctcttggggttacgaaagtcgcgdaatagcccat

ggtcttatccatggcttgcgggtagttaaggaaggtctgaagtag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 54 as follows:

MNPITHSFSHLGFSNAQSTSALAPGGNKVPNFVSRGRGKGVPLEHFNTADEYRLARQQGGVLKSIDGRE

FMLLLQKYTAAETSDEEFADLRAAIPRYSIDLAEPGQTKVLYRGISLPEKTAARLLNISWGYESREIAH

GLIHGLRVVKEGLK

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted. Furthermore, the protein of SEQ ID NO: 54 has been shown to be translocated by DC3000 in planta.

A twenty-eighth nucleic acid molecule encodes HopPtoL (ORF29) and has a nucleotide sequence according to SEQ ID NO: 55 as follows:

atgactactctgaccaccagacagatacaactcgcccacgcttggacatccgttcatacaggcgctggc

ctggccctggactgggtcgccgatgtggccgaaaaggtcgaggaaatcgccaccaaggccgacgccctc

agccgtgacttgcaccgcgcgcgcaacctgtcccgcagccttgggcgggtctcgacgacacccatgggt

atcggtttcttcggcttgtctcaggcaggcaagagctacctgatttccgctctggcggcggacgagaaa

ggccagttgctgacccggctgggtactcagcaactggacttcatcaagcacgtgaacccggtgggcggc

ggtaaggaggccaccggtctggtcacgcggttcacccgcaccgccgcgccaagtctggacccgcacttt

ccggtggagctgcgtctgtttcgcgaggtcgagatcgccatcattttggccaacgcctggtttgaggat

ttcgatcatcagcgcttgaacagccaagtcaccgatgcgcagatcgatgccctttgcagcgtttcgag

gggcaattggcagccgctccgacacctggcgtcagcagtgacgacgtggtgctgctatgggattacctg

gagcaccattacgctaacgccatgcgcccgctgaacgcccgttattggccttgcgtggtcaaactggcg

ccgcgcttgtcggcacgcgagcgcgctcaattgttcgagccgctgtggggcggcatcggcaaaatgacc

gaaacctatgagcaactggcctcggccctgcaccgcctggggctggcagagacagtttttgcgcccatc

agcgcgctggtcaccgagcgcgatgggcaactggtacaaagcaaaagcatcatcaacgtcgacattctc

agccgtcttggcggcagcgcggactcggccatcgaggtacgtccggccagtgaaggcactttgcgccct

gccgtgtcggtgaatcgggccgaactggcggcgctcaccaacgagttgatttttcgcctggataacgaa

ccggccaacgccatcgtcaatagcgtcgatctgctcgacttcccgggctaccgcagccggcagaagctg

atgagcatcaacgaggccagcgaagtcgacagcaatggcaccgccaacaatccggtcgccaggctgttg

ctgcgcggcaaggtcgcttacttgtttgagcgttacaccaacgagcaggaaatgaacgcgctggtgatg

tgcaccagcaccttcaagcagagcgaagtggtgagcgtcggtccggtactcaagagctggatcgacaag

acccaaggcaccagcccccagcagcgcgatggtcgggccagcggtctgatctgggcgttgaccatgtgt

gacggctttatcggcggcgcgctcaacggcgaggttgtgcagtttcccgaaggttgcgacaacatgctc

-continued

aaactgaccatgatcgagcgattcggcaacgaagactggatgaaacaatggggcagcacgcctttcaaa

aacacctatctggtgcgcaagccgcgcttcaagaccagcttcatcgagttggcggcggacggtgaagaa

cgcgcttacaacgactcatcgcactctgcgttacaggcattgcaacaagcgttcagcaacagtgaactg

gtcaagcgccatgtggcagaaccgcaggacgcctggcaggcaatgctgacactgaacgacggcggcatg

actcgtttcagctcggcgttcagcccgattgccaacatcgacttcaagttacagcgtattgccgagcaa

ctggacgagttgatggtgcaattactgccgcgcctggagcagtactacgaagccggtggcgaagacgaa

cgggccaggaagaaggttatcgccaacctgattgcccgcccgttcgcgaccacgccgcacggcaaacac

gtgcttggcgaactgctcggttacatgtcgttgccggaacagcagttgcgcgacctttacctgaacggt

gatttcgccagccctgccagcgacgccactgcaccggtgcaggccgtcggcaagcctgaagtggaatac

gacatattcggcgaggccatcgcagccactgccacggtggaaatacccgcggcaccggccgtagcgccg

caataccagagccacgaacaccgtttcgcccgagcggccttcgacctgtgggcaacgcacctgcgcaac

ctcagccgtcgccagcacctgctggacctgttggagctgcctgccgaggccatcgccctgctggtcaag

gaactggtggtctgcgccgagcgcctggacttgccattgcagctcagcaacgcgctgctcaagcgcgcc

cagagcggtgtgcgcaaagaaaacctggtgcagcgccaagtgctgaccgcgcaactgctgctcaacgac

ttcgccgcctggttcgggcacaccgcccagccggcgggtcagcggccaacgggcctgctgggtgccaaa

caaccgctgtttgctttttatcaaaaggaaatgccagggcgcttcccgcacctcgcagcgcaagccgac

gaccagagcgtgattttcgccgatgactggatttctggcattgccattcatacccagaaaaacgtcggc

caccgcaagggcaaagaaatcactcctgagcagaacgaggccatgggccgcgtcatccaggcgttcaaa

gcgagataa

The HopPtoL protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 56 as follows:

MTTLTTRQIQLAHAWTSVHTGAGLALDWVADVAEKVEEIATKADALSRDLHRARNLSRSLGRVSTTPMG

IGFFGLSQAGKSYLISALAADEKGQLLTRLGTQQLDFIKHVNPVGGGKEATGLVTRFTRTAAPSLDPHF

PVELRLFREVEIAIILANAWFEDFDHQRLNSQVTDAQIDALLQRFEGQLAAAPTPGVSSDDVVLLWDYL

EHHYANAMRPLNARYWPCVVKLAPRLSARERAQLFEPLWGGIGKMTETYEQLASALHRLGLAETVFAPI

SALVTERDGQLVQSKSIINVDILSRLGGSADSAIEVRPASEGTLRPAVSVNRAELAALTNELIFRLDNE

PANAIVNSVDLLDFPGYRSRQKLMSINEASEVDSNGTANNPVARLLLRGKVAYLFERYTNFQEMNALVM

CTSTFKQSEVVSVGPVLKSWIDKTQGTSPQQRDGRASGLIWALTMCDGFIGGALNGEVVQFPEGCDNML

KLTMIERFGNEDWMKQWGSTPFKNTYLVRKPREKTSFIELAADGEERAYNDSSHSALQALQQAFSNSEL

VKRHVAEPQDAWQAMLTLNDGGMTRFSSAFSPIANIDFKLQRIAEQLDELMVQLLPRLEQYYEAGGEDE

RARKKVIANLIARPFATTPHGKHVLGELLGYMSLPEQQLRDLYLNGDFASPASDATAPVQAVGKPEVEY

DIFGEAIAATATVEIPAAPAVAPQYQSHEHRFARAAFDLWATHLRNLSRRQHLLDLLELPAEAIALLVK

ELVVCAERLDLPLQLSNALLKRAQSGVRKENLVQRQVLTAQLLLNDFAAWFGHTAQPAGQRPTGLLGAK

QPLFAFYQKEMPGRFPHLAAQADDQSVIFADDWISGIAIHTQKNVGHRKGKEITPEQNEAMGRVIQAFK

AR

HopPtoL has been shown to be a protein that is secreted by DC3000. HopPtoL has significant homology, as detected by BLAST search (1e-21), to an SPI-2 regulated SrfC (see Worley et al., *Mol. Microbiol.* 36:749–761 (2000); GenBank Accession No. AAF74575, each of which is hereby incorporated by reference in its entirety).

A twenty-ninth nucleic acid molecule encodes HopPtoS2 (ORF30) and has a nucleotide sequence according to SEQ ID NO: 57 as follows:

```
atgaatataaatcgacaactgcctgtatcaggctcggagcgattgttgactcccgacgtgggcgtatct
cgccaggcttgttccgaaaggcattattctactggacaggatcggcatgatttttaccgttttgctgcc
aggctacatgtggatgcgcagtgttttggtctgtcaatagacgatttgatggataagttttctgacaag
cacttcagggctgagcatcctgaatacagggatgtctatccggaggaatgttctgccatttatatgcat
accgctcaagactattctagtcacctcgtaaggggggaaataggaacgccgctgtaccgagaggtcaat
aattatcttcgacttcaacatgagaattctgggcgagaagctgaaattgataatcacgacgaaaagcta
tcgcctcacataaaaatgctttcatctgcgcttaatcgtttaatggatgtcgccgcttttagaggaacg
gtttatagaggcattcgcggtgatttagataccattgctcggctctaccatctattcgatacgagcggc
cggtacgtagagcccgctttcatgagtacaactcgaataaaggacagtgcccaggtgtttgagccaggc
acgccaaacaacatagctttccagataagcctaaaaagaggcgccgacatttcgggatcttcccaagcg
ccctcagaggaagaaatcatgctacccatgatgagtgagttcgtcattgaacatgcatccgctctttcc
gaaggaaagcatttatttgtattaagtcagatttga
```

The HopPtoS2 protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 58 as follows:

```
MNINRQLPVSGSERLLTPDVGVSRQACSERHYSTGQDRHDFYRFAARLHVDAQCFGLSIDDLMDKFSDK
HFRAEHPEYRDVYPEECSAIYMHTAQDYSSHLVRGEIGTPLYREVNNYLRLQHENSGREAEIDNHDEKL
SPHIKMLSSALNRLMDVAAFRGTVYRGIRGDLDTIARLYHLFDTGGRYVEPAFMSTTRIKDSAQVFEPG
TPNNIAFQISLKRGADISGSSQAPSEEEIMLPMMSEFVIEHASALSEGKHLFVLSQI
```

HopPtoS2 has been shown to be a protein that is secreted by DC3000. HopPtoS2 has significant homology, as detected by BLAST search (1e-5), to Clostridium exoenzyme C3 ADP-ribosyltransferase, (Nolling et al., *J. Bacteriol.* 183: 4823–4838 (2001); GenBank Accession No. NP_346979, each of which is hereby incorporated by reference in its entirety). Further confirming that HopPtoS2 has similarity to ADP-ribosyltransferases, it was determined to possess an ART domain (pfam1129). In addition, HopPtoS2 has 20.5% identity to the HopPtoS1 as determined using EMBOSS software.

A thirtieth nucleic acid molecule encodes HopPtoS3 (ORF31) and has a nucleotide sequence according to SEQ ID NO: 59 as follows:

```
atgaatatcagtcctgtatcgggtgcccacggtagcagctacccttcagctcaatccacagcatcgacg
gcatcgaaaggtccctctggatcctttctcaaacagctcggcggctgtttttcaccctgcctgggtagc
agctctactggggccatactttctcccgctcatgagcaggtattgagccacacctattccagcaatatt
aaaggaaagttgcgcacgacgcccccaaaaggaccgtcgcccaggttgtctgacacacctatgaagcag
gcgctttcttcaatgatcgtacaggagcgaaaacggcttaaaagtcaacccaagtcattggcctcggat
atagaacgtccagacagtatgatcaaaaaagcgcttgatgaaaaagacggccacccgtttggcgagcgc
ttttcagacgacgaatttcttgcgattcatctctatacgagctgtctttataggccgatcaatcatcat
ctgcggtatgccccgaacaatgatgttgcaccggttgtcgaggcactgaaaagtggtttggcaaagctt
gctcaagaccctgattatcaagtgtctagccagcttcatagaggcatcaagcaaaagatgagtgatggc
gaggtcatgagtcgtttcaaaccgggtaagacctatcgtgatgaagcgttcatgagcacatcaactcat
atgcaggtttcagaagagtttacctccgacgttacgttgcacctgcggtcctcatcagctgtcaatata
ggcccctttcgaaaaatccatacgaggacgaagcgcttatctcgcccctgacgcctttcaaagtaacc
ggtctgcgcaagcaggacgataagtggcacgtcgatttgaacgagatagcagataattcagacgagtga
```

HopPtoS3 has an amino acid sequence according to SEQ ID NO: 60 as follows:

MNISPVSGAHGSSYRSAQSTASTASKGPSGSFLKQLGGCFSPCLGSSSTGAILSPAHEQVLSHTYSSNI

KGKLRTTPPKGPSPRLSDTPMKQALSSMIVQERKRLKSQPKSLASDIERPDSMIKKALDEKDGHPFGER

FSDDEFLAIHLYTSCLYRPINHHLRYAPNNDVAPVVEALKSGLAKLAQDPDYQVSSQLHRGIKQKMSDG

EVMSRFKPGKTYRDEAFMSTSTHMQVSEEFTSDVTLHLRSSSAVNIGPFSKNPYEDEALISPLTPFKVT

GLRKQDDKWHVDLNEIADNSDE

HopPtoS3 has significant homology, as detected by BLAST analysis (5e-3), to chicken ADP-ribosyltransferase (Tsuchiya et al., *J. Biol. Chem.* 269:27451–27457 (1994); Genbank Accession No. P55807, each of which is hereby incorporated by reference in its entirety). Further confirming that HopPtoS3 is an ADP-ribosyltransferase, it was determined to possess an ART domain (pfam1129). In addition, HopPtoS3 has 71.7% identity to HopPtoS1 as determined using EMBOSS software.

A thirty-first nucleic acid molecule encodes ORF32 and has a nucleotide sequence according to SEQ ID NO: 61 as follows:

atgaatattaacccttccctgggcgctcatggcagcgcctactcgtcgcctcaaagtgatacttcgaag

gccactggaaaagcacctgcgccttctttttttcaaacagttgggcggctgtttttcgccgtgccttggt

tcccatgcgtcaagcagccaacaactgtccgccagtcatgcgcagacgctcagtcagaattactccagc

aacattcaggggacgagccgcacacgccagccgagagcaccctcgccacgcctgtcagatacgcccatg

aagcaggcgctttcctcaatgatcgaacgcgagcgtttgcggcttcaaggtctttcgggaggaatgttc

tcgggcattgactccgccgatgccatgattggtcgagcgctcacgaagaaggattcaaacccaaaggct

gcgcgttttagtgatgatgagtttctcgccgttcacctctacacaacttgcctctacagacctatcaat

catcatcttcggtatcaacactag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 62 as follows:

MNINPSLGAHGSAYSSPQSDTSKATGKAPAPSFFKQLGGCFSPCLGSHAS

SSQQLSASHAQTLSQNYSSNIQGTSRTRQPRAPSPRLSDTPMKQALSSMI

ERERLRLQGLSGGMFSGIDSADAMIGRALTKKDSNPKAARFSDDEFLAVH

LYTTCLYRPINHHLRYQH

This protein has significant homology, as detected by BLAST analysis (5e-3), to chicken ADP-ribosyltransferase (Tsuchiya et al., *J. Biol. Chem.* 269:27451–27457 (1994); Genbank Accession No. P55807, each of which is hereby incorporated by reference in its entirety). Further confirming that protein of SEQ ID NO: 62 is an ADP-ribosyltransferase, it was determined to possess an ART domain (pfam1129). In addition, this protein has 51.3% identity to HopPtoS1 as determined using EMBOSS software.

A thirty-second nucleic acid molecule encodes ORF33 and has a nucleotide sequence according to SEQ ID NO: 63 as follows:

atgagctcgatcacgcacaccaacacgccgcaattggcggtcagcgattcacggggtctgccggtacgc

agtgtgcagttctatcgtggcgctgatggtcagcctgttgacgcgagggtgacgcagcactatttcgac

-continued

aaggccgggcgactgatcgccagtcgcgatccacgtttttccagtcgtttgaaatacggtgtctgtgcg

cctgtgaacctgatgcaaatcgtcagcttgtccggggctttgctgttatcgaaaagtgtcgattcaggt

tggcgggtgagcctgaacggcgaagcggggcagttagtcgacagctgtgacggacgtgacaacccgcgc

cagatcgaatacgacgggctgttgcgccctttggcgatcaacgaatcaggccgaatgaccgagcgcttc

acttatggcgggcctgccactgctgagcataaccagtgcaatcaactgattcgccatgacgatacggca

ggctcgcgcttgctgcgggactatggactgtcgggtagggcgttgagcgaaaaaaggtacttcctgcag

tcgcccgacagcccggactggccacttgccgagcctgatcgtgatgcactgctcgagccggtcggcctg

cagacgcgctgggctttcaacgcgcagggcgaggacctggcgcagactgacgcaaacggtaatgtccag

cgtttcagtcacggtgtggctgggcaactgcacgctgttgaactgaccctggccaatacggcacagcgg

caaacgctggtcagtgcaattcactacgacgcgttcaatcaggccgagcaggagacggcaggaaatggt

gtggtcagtcgctatgtgtatgatcaacaggacggtcggctgactgagctcagtgcgctatctgccgac

ggctcagtgttgcaaaaactgaactacagctatgacccggcaggtaacgttctactcatcaacgatgcc

tcgcaaccagaccggtattgcggcaatcagcgtatcgagccgataaaccgttactgttacgacacgttg

tatcagttgatcgaagccacggggcgggaggtcagaaacggggccagccatggtccggcgctacccggt

ctgcaacctctgccgacgctcgatccttgccaggtcagcaactacacacagcgttacagctacgacgct

gcgggtaacctgctgcaaatgcgccacgaaggcgcgcacaacttcacccgcaacatgcacgttgatccc

gacagcaatcgcagcctgcccgacaatgacaggtatgtggatttcgccacgagttttgatgccaacggc

aatctgctgcaactcgtgcgtgggcagaccatgagctgggatgtgcgtaatcagttgcggcaaatcact

accgtgcaacgtgaagacgcaccgaatgatgaagagcgctatgtatacgacggccagggccagcgctgc

cgcaagatcagcaccgcgcaggcatcaggtcgcacactgaccaatgaagttcgctacctgccgggactg

gaagttcggaccacggccgatggagaaactcttcacgtcgttacggctcaggcgggtcgcaacagcgtg

cgggtgttgcactgggaagccggaaaaccaggcgctattgcgaacgatcaggtgcgttacagcctgggt

gatcatctgggctcgagcacgctggagcttgatcagcaaggcggcctgatcagccaggaaagttattac

ccctttggcggcacggcctggtgggcggcgcgtagtgcagtggaggccaagtacaaaacagtgcgttat

tcgggtaaagagcgcgatgccagcgggctttattattacgggttcaggtattacgcgccgtggttgcag

cggtggatcaatcctgacccggcgggggatgtggatgggttgaatctgtacaggatggtcagaaataat

ccgcttgtttacgttgatgcgaagggccagcaacctgaacctgttccaaaaactattcaccagatctgg

ataggtgaaaacaagaatgccttgagagctcaggttagcaatatcaacagaaccgttgaaatggcttgg

gggtataaagtgaagttgcatctggaaacgaggacgccggaagcttattcggaaatcgaaaaggatctg

agatccgaagtggttctgcttcctgattcccaggtttttcaaaacttcaaggagaagccgctttatgcg

gcctatgaagatttccgaagaaacaatcagaattacgctttcgcggtagacgttttacgtatgcatacc

gttcatgatttgggcgggatttattcagatgtcgatgacgtttatgcaggtgcggagactggcggaatg

acgcagttgggggataatccgctgtttgcagaacctgatgaggttttgacgctggatcctgttcatgtc

ccttgggagccccagaattctgttgaaagttttatggtcaataacagctcatttgccgctcattcaggt

gcaggcgtcttacttgacatgatgggggaaggagcgaaacgatatgatgaagccgttgagggcggaagt

tatccggatccgacgggcatgaacggtataggtctaagtctgctctggaatcctaacccggcagtaaga

gttcgaacgttatcgaatgtagtaggccccggcttgtttacagacacactgcacgcttcggacacagca

tacggtgagcttttagtaatctgaaaggcgtcgtctttcaaaaacagccgttcacgtttgccgaccaa

atggccaggaagatgccgctgcatcggcatataaaaagcggcgcggcgcaaacctggcgctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 64 as follows:

MSSITHTNTPQLAVSDSRGLPVRSVQFYRGADGQPVDARVTQHYFDKAGRLIASRDPRFSSRLKYGVCA
PVNLMQIVSLSGALLLSKSVDSGWRVSLNGEAGQLVDSCDGRDNPRQIEYDGLLRPLAINESGRMTERF
TYGGPATEAHNQCNQLIRHDDTAGSRLLRDYGLSGRALSEKRYFLQSPDSPDWPLAEPDRDALLEPVGL
QTRWAFNAQGEDLAQTDANGNVQRFSHGVAGQLHAVELTLANTAQRQTLVSAIHYDAFNQAEQETAGNG
VVSRYVYDQQDGRLTELSALSADGSVLQKLNYSYDPAGNVLLINDASQPDRYCGNQRIEPINRYCYDTL
YQLIEATGREVRNGASHGPALPGLQPLPTLDPCQVSNYTQRYSYDAAGNLLQMRHEGAHNFTRNMHVDP
DSNRSLPDNDRYVDFATSFDANGNLLQLVRGQTMSWDVRNQLRQITTVQREDAPNDEERYVYDGQGQRC
RKISTAQASGRTLTNEVRYLPGLEVRTTADGETLHVVTAQAGRNSVRVLHWEAGKPGAIANDQVRYSLG
DHLGSSTLELDQQGGLISQESYYPFGGTAWWAARSAVEAKYKTVRYSGKERDASGLYYYGFRYYAPWLQ
RWINPDPAGDVDGLNLYRMVRNNPLVYVDAKGQQPEPVPKTIHQIWIGENKNALRAQVSNINRTVEMAW
GYKVKLHLETRTPEAYSEIEKDLRSEVVLLPDSQVFQNFKEKPLYAAYEDFRRNNQNYAFAVDVLRMHT
VHELGGIYSDVDDVYAGAETGGMTQLGDNPLFAEPDEVLTLDPVHVPWEPQNSVESFMVNNSSFAAHSG
AGVLLDMMGEGAKRYDEAVEGGSYPDPTGMNGIGLSLLWNPNPAVRVRTLSNVVGPGLFTDTLHASDTA
YGELFSNLKGVVFQKQPFTFADQMARKMPLHRHIKSGAAQTWR

This protein has significant homology, as detected by BLAST analysis (1e-128), to SepC insecticidal toxin (Hurst et al., *J. Bacteriol.* 182:5127–5138 (2000); Genbank Accession No. NP_065279, each of which is hereby incorporated by reference in its entirety). This protein also has significant homology (2e-128), as detected by BLAST search, to putative insecticidal toxin from *Yersinia pestis* (Parkhill et al., *Nature* 413:523–527 (2001); GenBank Accession NC_003143.1, each of which is hereby incorporated by reference in its entirety).

A thirty-third nucleic acid molecule encodes ORF34 and has a nucleotide sequence according to SEQ ID NO: 65 as follows:

atgccgatcaccgcgcagcagttgctgcagatactcccgagcgctggccagaaagccggcgtttttgca
cccgtcctgaacacagcgatgagcaagcaccagatcttgacgccgctgcgcatcgcggctttcatcgcc
caggtcggtcatgagtccggccaactgcgctacgtccgcgagatttgggggccgactccgcagcagctg
ggttatgaaggccgcaaggacctcggcaataccgtggcgggtgatggttcgaagtaccgcgggcgcggc
ctgatccagatcaccggccgggccaactatgccgaatgcggcgaggcgctgggcctagacctgatccat
cacccggaactgctcgagcagccggagcacgccacaatgtcggcagcgtggtactggagcagccgtggc
ctgaactcgctggccgacaaaggggactttcttcaaattacccgaagaatcaacggaggcaccaatgga
ctggcggatcggcaggcgctgtacgaccgggcgctgaaggtgctggcgtga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 66 as follows:

MPITAQQLLQILPSAGQKAGVFAPVLNTAMSKHQILTPLRIAAFIAQVGH
ESGQLRYVREIWGPTPQQLGYEGRKDLGNTVAGDGSKYRGRGLIQITGRA
NYAECGEALGLDLIHHPELLEQPEHATMSAAWYWSSRGLNSLADKGDFLQ
ITRRINGGTNGLADRQALYDRALKVLA

This protein has significant homology, as detected by BLAST analysis (3e-36), to a lytic enzyme (Nakayama et al., *Mol. Microbiol.* 38:213–231 (2000); Genbank Accession No. BAA83137, each of which is hereby incorporated by reference in its entirety).

A thirty-fourth nucleic acid molecule encodes ORF35 and has a nucleotide sequence according to SEQ ID NO: 67 as follows:

atgaatctaacagctttaggttcaaagctgtctcggtatcgcaagcagcttgcgatgagcgaggaagaa

gtgtgtgcggtcacccacatccccctgagcgcctgcagtcagttgaagccggctctcaggcgcctacg

ggtgatgaagtgcttatcctggccgatctctaccactgcaacttcaaattcttcatctcgaacgagccg

ctcgccccctttgagcagaccgaaatcctgtatcgcaggcacggagctgagttcatcaaggaggatcgt

agagccgtccaagaattcctgtacctctgcgaaacagaggacttcctgatgagtgagttgaaggctatg

aagctcgaatttccgctgccgcaggcttctgggaattttaagaatgatggaatccgagcggctgaagcc

tttcgccttttcaatcagcaccccacaaacgccgtgcctcgggatgtgtatcaggagattcgccaaacc

ggagtgcatgtgttccgtagaaagcttggtaactctaacatttcggggctttcctggctcaccccacg

gctgggaagtgcattctggtcaactacagcgaagacgtataccggcagcggtttagcgctgcgcatgaa

tttgctcacgctcttttcgatgcgcagggtggccccagtattacctactcccgtacgactaaggctgac

ctagtcgaagtgagagcaaacacctttgcctcccggtatctgatgccttcagaaatcctccgacagctg

cccaaccctgagcaatggacacaggaaaatacccagtattgggctcatgagttgcgagtcagctgcgtt

gccttgggcataggtctgaagtccgagggcttaattagcgagcaagcattccagaggataaagtcgtac

cgcgttcctcgtgaactgaagattgacccagaattgccggcccaattgacgacgcaacagcgtgagcga

aaggctaagttactggaaaaggggttatctgacagctacgtcgcactgtgcctagacgctcagagccgt

ggcatcatcactcaaggtcgattggctgaagccttgcttagtgacttgggaggccttcaagagctgctc

agcctttatggaagatcgcgcaatggccattga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 68 as follows:

MNLTALGSKLSRYRKQLAMSEEEVCAVTHIPLERLQSVEAGSQAPTGDEVLILADLYHCNFKFFISNEP

LAPFEQTEILYRRHGAEFIKEDRRAVQEFLYLCETEDFLMSELKAMKLEFPLPQASGNFKNDGIRAAEA

FRLFNQHPTNAVPRDVYQEIRQTGVHVFRRKLGNSNISGLFLAHPTAGKCILVNYSEDVYRQRFSAAHE

FAHALFDAQGGPSITYSRTTKADLVEVRANTFASRYLMPSEILRQLPNPEQWTQENTQYWAHELRVSCV

ALGIGLKSEGLISEQAFQRIKSYRVPRELKIDPELPAQLTTQQRERKAKLLEKGLSDSYVALCLDAQSR

GIITQGRLAEALLSDLGGLQELLSLYGRSRNGH

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A thirty-fifth nucleic acid molecule encodes ORF36 and has a nucleotide sequence according to SEQ ID NO: 69 as follows:

atgaatatcaacccctggcttcttcattacagaatcaacagcgcactctcttaggcccgccccccctc

aattcatctgctgctctgccgatcaagatccctgtggcgcatgataaagcgcgtgaccctaacgctgaa

ttctataccaccgaggaaacgccctggtttgccggctacaaaaagtcggaggcaggacgcgctatttta

gagaaaatgtctgagaaggaagcaaaagatatccgaggcgagtatctgggaaactacatgaaagccttt

gacgaaaccatatgtcgtatgtacgacaattttcacgatttcaaacagcagctttttaccttaatacg

gagctgtcaaaaaagcatttcggcttcacgctgggctttaatcaggacattcaggtgaccgacccggac

gaggtactcaccccggcagagttcacgtacctgaccgagaagctgaacgaacgccaacaactgaaagag

-continued

gatctgcgtgcgcacgcaaaaattgtgatgacgctgctcgaccattacaccgaaaaattcgataaccgg

cacaccctcaatctggagagttacagcaaggtcatcgactacggacagatcttcagccgcaatcatatt

ggcaatttcatggacacgattatctaccagatcgagcgcaatgcgccgaagcgtgaggaagaaccaaaa

cctctggttgatgtgcacgcttga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 70 as follows:

MNINPLASSLQNQQRTLLGPPPLNSSAALPIKIPVAHDKARDPNAEFYTT

EETPWFAGYKKSEAGRAILEKMSEKEAKDIRGEYLGNYMKAFDETICRMY

DNFHDFKQQLFYLNTELSKKHFGFTLGFNQDIQVTDPDEVLTPAEFTYLT

-continued

EKLNERQQLKEDLRAHAKIVMTLLDHYTEKFDNRHTLNLESYSKVIDYGQ

IFSRNHIGNFMDTIIYQIERNAPKREEEPKPLVDVHA

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A thirty-sixth nucleic acid molecule encodes ORF37 and has a nucleotide sequence according to SEQ ID NO: 71 as follows:

atgggcctgatcggcgtcaaacagaacaaaccgcaacaggcgcagacctacctgacgcgcctgcaagcg

ctgtcgccagcgccctggcaggcggtgcagctggagcaggacattgccctcggccagccgcaaaatcag

gcgctgctggatgatgcccgacgcctggccgacgccggtgagcgtgacaaggcgaccggggtgtttcgc

cagttgttcaacggccgtttgcctcaaggcactgtcggccgcgagtactacaccaacctgggcttcaac

aatgcggactggcccgaggcgcgcaagggttttgaacgcctgatgcggcagaaccctgacgactcgatt

ctggcgctgttctttgccaagcacctggcccgccgcgaagacagccgcgccgaaggcatcgccgctctg

gcgcgcctgagcactcatccggacatcgccggcgatgccgatcagagctggcgcatggcgctggtctgg

atcggcccgcctgcggctgcgcaagtgccactgttcgacgcgtttctcaaggttcatcccgacgatcag

gaaatccgcgaccagttgaacaagggtcgccagcagcatgccagcggcgctgcctcaggctggcagcaa

gacccgctggtggcgcgcggcttgaaggcgctggaaaaaaatgatcatgtggcggccgaagaagccttt

gccgcccgcctgaaaatcaaggcggacgatgccaacgtgcttggcggcctgggcgtggtgcgtcagcag

cagaaccggttgcctgaagccgaacaattgctgacccgcgccacgcgccagcagggcggtgcgcgctgg

aaaaacgcgctggaaaacgtacagctctggacctcgctgcaagaggcccgtgacctgcaggccaaaggg

cagaccggcaaggctcaagcgttgctggctcaggcgcagcggcaaaaccctgacaatatcgacgtgcgt

ttgaccctggccgacgtgcaggtgcaggccgggcaactggacgccgcgcaagcgggctatcgtcaggta

ctggcgacccagcgcggtaatccgcaggcaatccgcgggctgatcaacgtgctggcccagcgtggtcag

gctgatgaagcgttgcgcctgctcgacacattgtcgccaggcgaacaggccaaactgggcgacagcggt

cgcttcaaggcgctgcgctccacccaggtggcgcggctggccgagcagcgtggcgatgttcgcgctgcc

caggtggccttgaaagacgcggtgaagaacgacccggacaatgtctggacgcgttttgatctggcgcgc

ctgtacctcaagaccgacgaagcgcccaaggcccgcgcgctgatcgacgagctgctcaaggctcagccc

aacaatatcgatgcgctctacaccagcgcgctgctgtcagtggaaatgggccagtggcaggacgcgcag

accacgtttacgcgcatcccggttgatcagcgcacgccggacatgaaagcgcttgctgacgaagtcacc

atgaccgtgcagatcaatctggccatcggcatcgcccggcgcggtcagcgccaggaagcgttggcgctg

ctcgatcgcttgcaaccggtcgccagcggcagcccggagcgtcaactcacgctggccagcgcttacatc

gatgcgggcgagcccgcgcgcggtcgggaaatggcccgtgcggccatcgctcaggcccctttgccgtcg

gccgacctgatgctgcaatacgccggtctgctgctcgcagcgggcgatgacgtgcaggtcaatgcgatc

-continued

ctgcgcaacgtgcagggtcagccgatgagcgtgcagacccgcaaacgttttgatgacctttgtaccgc

taccgcattcgtcaggccgatctgctgcgtgaaggcggtgatctggcgggcgcgtacgacacgctggca

cctgctttggcgcagcgcccggacgacattcaggcggtgtcggccttcgcccgcatgtacaccgccaat

ggcgacagcgcccgagcgttcgagctgtacaagcctttgttgcagcgccagcccaatgacccgcaagtg

ttgctgggcgcagccgatgcggcggtcaaagcgcatgattatggctttgccgaaaaagccctgagccag

ttccgcaaactggagcgtaacgacccgcagaccctgacggaggccgcacgtatctaccaaagcatgggg

cagaccggcgcggccaccgagttgctgcgcaaggccgtggccatcgaacagagtgaaaaacagcgcgcg

atggctgtgcaggctgtgtcgaccagcaccacgtcgtccaacccgtttgcgacgggcggctcacgtagc

ctggcggcggcttcggctattccggctccggctcaggtgtcgctcagcggtgggagagcgcttgaaaca

aacagtgcgcctgaaatatctgccccgcgtgacaccgcttatcccggccagatcgccgcaccacaaccg

ctgtctgccgcacgtacgcaaagtgtgcgcggcaatccgttcatggcagccaccgaccgcgatcaggcc

agcagcgcacagcaggcgctcaatcgcattcttgagcagcgcagtggcttcgtcagtcagggcctggcc

gtgcgcagcaataacagcgagtcgggtctgagcaaactgaccgtggtcgagaccccgctagaggtcaat

ttgcctgccggtgataaccgggtggccgtgcgcgtcacgccggtgtcgctgaatgctggcagcttgaag

tcagatgcaggtgcccgttttggcggtggcaccagcggtgctgccggttcgcagagcgacaagggtgtc

ggtctggcggtggcgttcgagcgccccgaagaaggcctcaaggccgatatcggcaccacgccgatgggt

ttcaaatacaccacggttgccggcggcgcgagtgtcgaccggccgttggctaacaacccggacctgcgc

tacggcctcaacgtgtcacggcgtccggtgacggacagcgtgacttcgtttaccggttccacagacgag

cgcagcggcctgtcctggggcggcgtcacggccaacggcgggcgcggtcagctcagctatgacgaccag

accatcggcggttatggctacggctcgtggcacaaactggttggcaacaacgtgaaatccaacacccga

ggcgaagtgggtggcggcgtttactggtacctgcgcaatgccgaggacagcaaactgaccgcaggcctg

agcctgatgggcatgagctatgacaatgaccagagctacttcacgtacggccacggtggctatttcagc

agcctgatgggcatgagctatgacaatgaccagagctacttcacgtacggccacggtggctatttcagc

ccgcagagcttctatgccatcggcgtgccggtgatgtgggcacagcgcaccgagcgtttcagctatcag

gtcaagagctcggtcggggtccagcacttcaagcaggacggcgccgaattcttccccgacgacagcacg

ctacaggccgcttccgcccagcgctacacagggcaaagcaaaaccggaattggctacaacctgagcgcg

gcaggcgagtacaagctcgattccagcctgttcatgggggccagtctgggcctggacaatgcccgggac

tatcgccagttcagcggcgcgctttacctgcgttacatgttcgaggacataaccggcccgatggcactg

ccggtcagcccttaccgttcaccttattccaactga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 72 as follows:

MGLIGVKQNKPQQAQTYLTRLQALSPAPWQAVQLEQDIALGQPQNQALLDDARRLADAGERDKATGVFR

QLFNGRLPQGTVGREYYTNLGFNNADWPEARKGFERLMRQNPDDSILALFFAKHLARREDSRAEGIAAL

ARLSTHPDIAGDADQSWRMALVWIGPPAAAQVPLPDAFLKVHPDDQEIRDQLNKGRQQHASGAASGWQQ

DPLVARGLKALEKNDHVAAEEAFAARLKIKADDANVLGGLGVVRQQQNRLPEAWQLLTRATRQQGGARW

KNALENVQLWTSLQEARDLQAKGQTGKAQALLAQAQRQNPDNIDVRLTLADVQVQAGQLDAAQAGYRQV

LATQRGNPQAIRGLINVLAQRGQADEALRLLDTLSPGEQAKLGDSGRFKALRSTQVARLAEQRGDVRAA

QVALKDAVKNDPDNVWTRFDLARLYLKTDEAPKARALIDELLKAQPNNIDALYTSALLSVEMGQWQDAQ

-continued

TTFTRIPVDQRTPDMKALADEVTMTVQINLAIGIARRGQRQEALALLDRLQPVASGSPERQLTLASAYI

DAGEPARGREMARAAIAQAPLPSADLMLQYAGLLLAAGDDVQVNAILRNVQGQPMSVQTRKRFDDLLYR

YRIRQADLLREGGDLAGAYDTLAPALAQRPDDIQAVSAFARMYTANGDSARAFELYKPLLQRQPNDPQV

LLGAADAAVKAHDYGFAEKALSQFRKLERNDPQTLTEAARIYQSMGQTGAATELLRKAVAIEQSEKQRA

MAVQAVSTSTTSSNPFATGGSRSLAAASAIPAPAQVSLSGGRALETNSAPEISAPRDTAYPGQIAAPQP

LSAARTQSVRGNPFMAATDRDQASSAQQALNRILEQRSGFVSQGLAVRSNNSESGLSKLTVVETPLEVN

LPAGDNRVAVRVTPVSLNAGSLKSDAGARFGGGTSGAAGSQSDKGVGLAVAFERPEEGLKADIGTTPMG

FKYTTVAGGASVDRPLGNNPDLRYGLNVSRRPVTDSVTSFAGSTDERSGLSWGGVTANGGRGQLSYDDQ

TIGGYGYGSWHKLVGNNVKSNTRGEVGGGVYWYLRNAEDSKLTAGLSLMGMSYDNDQSYFTYGHGGYFS

PQSFYAIGVPVMWAQRTERFSYQVKSSVGVQHFKQDGAEFFPDDSTLQAASAQRYTGQSKTGIGYNLSA

AGEYKLDSSLFMGASLGLDNARDYRQFSGALYLRYMFEDITGPLALPVSPYRSPYSN

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted. This protein also has significant homology (e=0), as detected by BLAST search, to cellulose synthase from *Pseudomonas fluorescens* (Spiers et al., *Genetics* 161:33–46 (2002); GenBank Accession P58937, each of which is hereby incorporated by reference in its entirety).

A thirty-seventh nucleic acid molecule encodes ORF38 and has a nucleotide sequence according to SEQ ID NO: 73 as follows:

atgaaactgatacgacagatccgctcgcagggtcgtcagtcgcccttgttcgaggaccttgcccagctc

gaggggcgcaagcgtcaatggctggccgagcgcgccgtgcagttcgcactgggcttgcacggccgccgg

ccagaggtcgataacccccttcaaaggcaaactgcgtgaagacctgtgctgcatcatgttcgatgacctg

tcgctgcacaccctggtcgagcgttacgcggccagtgaagccctgcgacgacacgacagcgagtacttc

agcaaactgatcgccacgacacgaaataccgtggaacggcgcatcgtctttcacgggctgctggaacac

ttcgacaggctgttgcctatcgaaaagagcatctaccaactcaactaccgcagcgttcaatacgcgcac

ctggagcaggaagaagccctgtacggcaaactgataatggaacaacccattagtgcactgctggaagtg

cacacgcctgagtggcttcttgagaatctgtcttcgtttgagttttcgattgattga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 74 as follows:

MKLIRQIRSQGRQSPLFEDLAQLEGRKRQWLAERAVQFALGLHGRRPEVD

NPFKGKLREDLCCIMFDDLSLHTLVERYAASEALRRHDSEYFSKLIATTR

NTVERRIVFHGLLEHFDRLLPIEKSIYQLNYRSVQYAHLEQEEALYGKLI

MEQPISALLEVHTPEWLLENLSSFEFSID

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A thirty-eighth nucleic acid molecule encodes ORF39 and has a nucleotide sequence according to SEQ ID NO: 75 as follows:

atgcgactgactactaaaggccgatacgctgtgacagccatgcttgacctggcgttacatgcgcagaac

gggccagtgtctctggccgacatctccgagcggcagggcatttccctgtcttatctcgaacagttgttc

-continued

gccaaactgcgtcgcggcaatctggtttccagtgttcgtggtccgggcggcggttatcagctgtctcgt

gacatgaaaggcatccaggtcgcccaagtcgtcgacgcggtcaatgaatcggtcgatgccacgcgttgt

caggggctgggtgattgccacgctggcgatacctgcctgacccaccacttgtggtgcgatctgagccag

cagattcacgaatttctaagcggtatcagcttggcggatcttgtcactcgccgtgaggtacaagaagtc

gctcagcgccaggatatgcgccgtggtcataaccacacgtcgcaactgggtaagatcgaaacgtccgcc

gtcgaatga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 76 as follows:

MRLTTKGRYAVTAMLDLALHAQNGPVSLADISERQGISLSYLEQLFAKLR

RGNLVSSVRGPGGGYQLSRDMKGIQVAQVVDAVNESVDATRCQGLGDCHA

GDTCLTHHLWCDLSQQIHEFLSGISLADLVTRREVQEVAQRQDMRRGHNH

TSQLGKIETSAVE

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A thirty-ninth nucleic acid molecule encodes ORF40 and has a nucleotide sequence according to SEQ ID NO: 77 as follows:

atgaataccgtcagaaaacccataacaccacggatgctcagcatgaccgataaaaacggcacccatcga

caacgacgtgctgcactgttccccaaaaccccggcgaccgccaccagcctgtgccctttcagagggcct

aatatcgccatcgtcccggtgcgctatgcgctggatcgctcgcgctatgacgctgaccccgcgcaactg

aagccactgcccaaagacggccaatgggcccacctgccgacgctgaaaactcgcagttacaccttacgc

caactgtacgacggctacgtttacgtgttcgacgaaacggccggcacgttgcacgaatacgcagcctca

gccagcgacggccatctgagccgcatcgtctggaccgatgcacacatcggtaacgaccagcgaagcggt

gccggtgaagggcaacccttttgtgctttacccgcgtgaccaccgcctgcacatcgccttttctcccctg

caatggacatggcgaatgtgcgagcacatgcgctcccacgccccaagccgcgcgttgtggatgaaggcg

ctggacctggccagctactgcctcaccatggccgaaccggacaccctgccgctggatcgaatcgccgag

gccgtggcggatatcgacaaagactgtgttgtggaagatggccgttttgcagattcggcgattcccagt

gttcgcccgccatcagaaggtgcagaaccctatccgttatgggcaccgctgggcgccgatgtcttctgg

cagggcagcgtctacgatcaggacagctctctggtcattgccctcaatgacccgctcgccgttttcaac

gacttgggcatgcagctggcggccgatcaggcggcttttcgggaatggcaaagcgcccacgaacacaag

atccagattgcccagaccgtcgccacgctgtgcggtgcagagagcgaagcagagaagctgccagcatcg

gtgcgcggtgatgcgctgcgcacgcatcagtacctgagcgaggtcgaagcctactttgaacaatgcatt

cttgaagaagcacagatcagcagtagcaacgttcctggagattttctgctgctgccggacatgttcaag

agcctggacatgcgcaaatcgatcgaaacacgttatggcagcgcgccgaccgatgagggcgcgcaggcc

tggaaagatcgccacaaatggcggcgcgaggtcgatctgagcagtgcgcgtcagtacctttgcagcac

ctgccgaccggagacaaacgcctgcaacaggtgcgtgacacgcaaagcgatttccagcactgggcggca

catataggcaccgaaccgctcaagctgttcatcgacaccacacacccgaaaaccctgctgtatttgcag

acgatcatgctcaatctgcagatcatctatgcgcattacagcgccgcaaatgcctggctcgccgagcag

gaagccaacaccagcagcctgtttggcaccctgcgttatggtttttcgccagcgctcaagcacgccctg

catcaggaagccgacgcactgctgaacggcctcggcgacgtcactaatctggccacgcgcatcggtgaa

ctcaatggcgtgctcaaccatcagggttttgccgacaagccgtggatgaaggcgctgaaacagcctgtt

caagacaccttcaaagccctcggcgaactggccagcggtgccggcaaagccaggtttgaaagtgtatta

-continued

ctggcatgggtgcccatcgacagccgcatggcccttggcaagcagcagaacatcgttgcgttgcttcgc

accctgctgatcggccagatattgctcgactcgacagcacgcgtcgcgatcaatgagcagacagtgacc

aagctcaaacagtgggtaagtgagtggcaagtcctcaacaagcaaatcagcgagctggtgcgcagttgg

caatacccgaacgcctacaacacgcgccaaagcaccgctcgcaaattgcaggcccataaacacaaactg

cgcgttcacgaactgagcatccctgccctgctcgactttcagaacaacgaatacgccaagctattgcag

gacgagattcgtcagtacttccagtctggcaaaaccctcgccacggactggctcgcccgcgccaaaggc

tggaccgaccgactgggcggcgttgctggcacgatcacctggggcgtggtcatgcttaacctgatcaat

accgccttcctctatcgggaccttacccgggacggggatttcagtaccaaggacattggcaaggtgacg

tatggattggggtacagcttcaatctgttgatggcggtgtttgtggacgcgccgtggagcatcataagg

gacgcaacgccagcgctgatcgatggcaagaatgtggccattctggacaggtccagtgcgtactggaaa

gccaagggaaatgcagcgtggggtgatgcgatacgtgggttcagggtttcgatggtggcgatgggtggg

tttgggcttgcggcggttacgcttgaattatttgatgttacagatgattttcacgcagctaaaacatca

gaagaaacatatggaattggcatcaaggggttttccgtagtggtgatgggattgggtgctgcggcccag

ctaatggcaggcatttctcccgctggcgtttttacgattatcgcaatgagtccgtggttcagcgtagcg

ctactggcagcaggcttgatttatctttttgctacgatggcccttaattacttcaagcaagacagtgtc

ggctggtggctacgcaagtgctgttggtccataacccaagactatcgctatgctgagactgcggaaggt

aagcatgacgaagtgcgcgcgctgatggaaataaaattatctccgcaggtccatgtaaaaagcaccgtg

aattatgaaaaccgttatcttggcaaaaacgatcactacagcgtagcggtacaaaatggcgcgggggta

caagtgcgcttgccgaatcttctacgcgggctgtccgtgcatttcaatatcgttagtagcaagagacca

tggggcgtgctgcccgtagaaaaaatagatcagccgatacatgaagcttttctggaccacgggcaattc

aggaaagtcgaacagttcgggatgtttaccaacaagcctgctggcaaggcgagtgaagactatacctac

ccccgcatgccacctgaaaacgaagacctcatctgggaaacctgggtgccgctcgacaaggacgcaacg

tatcttgagttgcaaatctggtacccggccaatcttttaaatcctggcggagacgatagaagctatctg

tttcagatggagcttggcacaaaaggcgataccgctattgacggcctggctgcagtggaactcgaggta

aaggcatcaagcaggattggcgctctgaccctagaagtcgcagagggcacacctgtatga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 78 as follows:

MNTVRKPITPRMLSMTDKNGTHRQRRAALFPKTPATATSLCPFRGPNIAIVPVRYALDRSRYDADPAQL

KPLPKDGQWAHLPTLKTRSYTLRQLYDGYVYVFDETAGTLHEYAASASDGHLSRIVWTDAHIGNDQRSG

AGEGQPFVLYPRDHRLHIAFSPLQWTWRMCEHMRSHAPSRALWNKALDLASYCLTMAEPDTLPLDRIAE

AVADIDKDCVVEDGRFADSAIPSVRPPSEGAEPYPLWAPLGADVFWQGSVYDQDSSLVIALNDPLAVFN

DLGMQLAADQAAFREWQSAHEHKIQIAQTVATLCGAESEAEKLPASVRGDALRTHQYLSEVEAYFEQCI

LEEAQISSSNVPGDFLLLPDMFKSLDMRKSIETRYGSAPTDEGAQAWKDRHKWRREVDLSSARQYLLQH

LPTGDKRLQQVRDTQSDFQHWAAHIGTEPLKLFIDTTHPKTLLYLQTIMLNLQIIYAQDSAANAWLAEQ

EANTSSLFGTLRYGFSPALKHALHQEADALLNGLGDVTNLATRIGELNGVLNHQGFADKPWMKALKQPV

QDTFKALGELASGAGKARFESVLLAWVPIDSRMALGKQQNIVALLRTLLIGQILLDSTARVAINEQTVT

KLKQWVSEWQVLNKQISELVRSWQYPNAYNTRQSTARKLQAHKHKLRVHELSIPALLDFQNNEYAKLLC

DEIRQYFQSGKTLATDWLARAKGWTDRLGGVAGTITWGVVMLNLINTAFLYRDLTRDGDFSTKDIGKVT

-continued

YGLGYSFNLLMAVFVDAPWSIIRDATPALIDGKNVAILDRSSAYWKAKGNAAWGDAIRGFRVSMVAMGG

FGLAAVTLELFDVTDDFHAAKTSEETYGIGIKGFSVVVMGLGAAAQLMAGISPAGVFTIIAMSPWFSVA

LLAAGLIYLFATMALNYFKQDSVGWWLRKCCWSITQDYRYAETAEGKHDEVRALMEIKLSPQVHVKSTV

NYENRYLGKNDHYSVAVQNGAGVQVRLPNLLRGLSVHFNIVSSKRPWGVLPVEKIDQPIHEAFLDHGQF

RKVEQFGMFTNKPAGKASEDYTYPRMPPENEDLIWETWVPLDKDATYLELQIWYPANLLNPGGDDRSYI

FQMELGTKGDTAIDGLAAVELEVKASSRIGALTLEVAEGTPV

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fortieth nucleic acid molecule encodes ORF41 and has a nucleotide sequence according to SEQ ID NO: 79 as follows:

atgtgcctggtggcgagcctgtcggtgctggcaggcatgaccgatgccatcggcttcatggccaccggc

gatttcgtctcgttcatgagcggcaacaccacgcgccttgcggtggcgatcagtgatggcgatttgagc

gtcacactccgtctggccctggccatctttgcgtttattgccggcaatgcactgggcgttgtcgttgcg

cgcctgggcaaccggcgcgccctgcccttactgctggctatcgccacgctgttgtgtgccgctgcggct

tggccgttggcgaacaatatgcttgccctgatctgggcgattctggcgatgggcatgctcaacgccgct

gtcgagcaggtcaacgggctgccggtgggcctgacctacgtgaccggcgcgctgtcgcgactggggcgc

ggtctgggccgctggatgctcggcgaacgccggatggctggcgcattcaactggtcccgtgggccggg

atgttcattggcgcagtgatcggcgcgttgcttgaacatcgtctggggctcaatgccttgctggtcagc

gccagcctgtcagcgttaatggcgctggtgtcgctgaaaatcccgcatcgctggcaacgtcagtacatg

ccgcgctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 80 as follows:

MCLVASLSVLAGMTDAIGFMATGDFVSFMSGNTTRLAVAISDGDLSVTLR

LALAIFAFIAGNALGVVVARLGNRRALPLLLAIATLLCAAAAWPLANNML

ALIWAILAMGMLNAAVEQVNGLPVGLTYVTGALSRLGRGLGRWMLGERRD

-continued

GWRIQLVPWAGMFIGAVIGALLEHRLGLNALLVSASLSALMALVSLKIPH

RWQRQYM

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-first nucleic acid molecule encodes ORF42 and has a nucleotide sequence according to SEQ ID NO: 81 as follows:

atgagagggcttggtgttctgagcatgaaccaccagtttcagggcaataccctgttcaaagaaataagc

ggtaccagcttttccgcgccctacatcacccatcttgcgggccgtctccttaacgagcacccagaggca

tcggcgaacctcttgcgcgctatgctggtgaatcatgcgtcattgtctagcgaggtcgagacgactttc

tccgacgacatgaggaagggctacaaagctaataaggcgacccacaaccgtgaaatatcgcgcgatgtg

agtggttacggccaagtgaatgaggcagacctgtttcggtcttccgaccattgcgttgtgctgatgtgt

gaagagtccattgagaaggactcgtgccagttctacgaactgcctttgcccacttcgtttcttcgcagg

gctagaggggcaaggcacctgagcgtcacgctggcttattctcctgccgtcaggacaactcggttggac

tatctggcaactcagatcagttatcgcctagtgaaaggttcgtcgcttgaggaagtccaggcctcgttt

-continued

aactacgacaagcaggacgaaacgaagacccgtggagatgacgctgagcagaatcgagacatcactgct

cagttgagaagccgcgggaccgtccagtcctcgcggtggacgttcaagaagcgaaatccagaagaaaaa

tggtttgtagttgtgatccgccaggatcgggaatggaatcatcccgacgtgctggatcgagaatcttac

gccctggtggtaacagttgctgatcgtgacaacgaacacgcgcagttgtatgccgaaattcaagccaag

ctgacgcttcaaaatcaggtgcgtgaagaggcaaggcagcgggctgttctgtaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 82 as follows:

MRGLGVLSMNHQFQGNTLFKEISGTSFSAPYITHLAGRLLNEHPEASANLLRAMLVNHASLSSEVETTF

SDDMRKGYKANKATHNREISRDVSGYGQVNEADLFRSSDHCVVLMCEESIEKDSCQFYELPLPTSFLRR

ARGARHLSVTLAYSPAVRTTRLDYLATQISYRLVKGSSLEEVQASFNYDKQDETKTRGDDAEQNRDITA

QLRSRGTVQSSRWTFKKRNPEEKWFVVVIRQDREWNHPDVLDRESYALVVTVADRDNEHAQLYAEIQAK

LTLQNQVREEARQRAVL

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-second nucleic acid molecule encodes ORF43 and has a nucleotide sequence according to SEQ ID NO: 83 as follows:

atgggcattggcggtttgcttaaacctttggtcgatttttaccgaagttgccgaccttacgcaccaag

atttcctcgccttccatcagctacgcgcgtttgcaaagcgatgcgtcccaggtacgcagtaaattggga

ttgggtgagcgcagcgtgctgggttatgaagcgctgatcgccgagttcaaggcgtgcggggcggttctg

gtgcccgttctttggggacaaaagcagcaacacaagaatgcgttgcacattctattgccggcgtcagat

gtcacctttgtcttcgtcaacctggataccaagctggaagacttcaagttttggatggcccacgagtta

gcgcatgtctacactcctgagcttgcgggtagtgacgaggggaggattttgcggatgcctttgccggt

gccctgctgtttcctgaggcttgcgtgcagctagcgtatgccgaggcggcgcaagcgcctagcgcagct

ggggaggtgagtgtccttcagcagcatgcccggcatcaccaaatttcactgaacacggtgttccagcag

gcgcagggatatgcggcggaaaacaatctgccatccttacgggtaccggaaaggacaattcacgcggtg

cgcaacatctccacgccgcagttggtcagtacgatcctgtttgatccgactccacccaaaccggcgcaa

tacattgccgcagcgtcgaatgtgtttcagtctgagttcttcctggcgctgaaacgcatgattcgcgag

cacgggacgggcccgtcgtatgttcagcaaatcatggatgtatcactcagtgatgcctccgcgctttac

ggcgagctcgcgcgttga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 84 as follows:

MGIGGLLKPLVDFLPKLPTLRTKISSPSISYARLQSDASQVRSKLGLGERSVLGYEALIAEFKACGAVL

VPVLWGQKQQHKNALHILLPASDVTFVFVNLDTKLEDFKFWMAHELAHVYTPELAGSDEGEDFADAFAG

-continued

ALLFPEACVQLAYAEAAQAPSAAGEVSVLQQHARHHQISLNTVFQQAQGYAAENNLPSLRVPERTIHAV

RNSSTPQLVSTILFDPTPPKPAQYIAAASNVFQSEFFLALKRMIREHGTGPSYVQQIMDVSLSDASALY

GELAR

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-third nucleic acid molecule encodes ORF44 and has a nucleotide sequence according to SEQ ID NO: 85 as follows:

atgaagcagctcgcggcaggcagcaatgtgcatgttcttgaaaatgagtctttccagatagataaggtg

cgctttttgggggccacagcttggacagatttcgcaacaggtgaaagcgtgtaccaagcgtcccaggag

gcaaggcgaggcatgaatgactttcgcttgatccgtgcaggcgagggttaccgcgcattgagcatcagt

gatgtgatcagtcgaaatcatcgaacttacgagtggctcaaggaagagctcgccatggagttcgatggt

cagaccattgtcatcactcatcattgcccgttggtcaattactgtggcccagagcagggctcaccgcta

atgcctgcttattcaaatgattggccagaactcgttcgtcaggctgatgtgtgggtctttgggcacacg

cacagtcatgtcgatgtcatggtggaaggatgccgactcattagtaaccctagaggttatccaggtgag

agttgcggctttgccaatgactttgtggtcgatattaactag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 86 as follows:

MKQLAAGSNVHVLENESFQIDKVRFLGATAWTDFATGESVYQASQEARRG

MNDFRLIRAGEGYRALSISDVISRNHRTYEQLKEELAMEFDGQTIVITHH

-continued

CPLVNYCGPEQGSPLMPAYSNDWPELVRQADVWVFGHTHSHVDVMVEGCR

LISNPRGYPGESCGFANDFVVDIN.

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-fourth nucleic acid molecule encodes ORF45 and has a nucleotide sequence according to SEQ ID NO: 87 as follows:

atgacgctgacgcagcgtcaggcatggcatcgcgaggcacagcggtttggcgagcaggtggtgaacatg

cgcaaagccagcaaggcgcacttcggccaggcggaaaatgacagccgcacctatccggcgcgctttatc

gaccagcaactggctcaactgctgaaccggctatccatcgctgcaacggcgcaacagatcaatatttca

ctgacctacaggacgggcaccgaagtgctcgaaattcccggcgcgcctgtattgccagaaaccgagacc

gagaacgtttcactcaggcaactggtgcatacccaggccctgcgcaccaaggccaaggatgccgtgctt

ctacgcgctgtcgacgccgaaggcgtccccttgcgcacttggacaagcaggccgtaaccgagctgatt

gccacgctggaagatcaccgatacctcagtgattaccttgacctgcacctgaaaacctcggcgtatgca

cagcagctcaagcggtcagaaaaagccatgttgcaagctcagatgaagatggcgctgctggagatcgag

caacaggcttttgcaccagccggtcgcgagtggatcaaggctgtgctggattcgccagcccccaagga

cgtcgaaccatggcaggggaaagcattgaagtccgtttttcagcgtcaaccaattcaagatgaccaat

gtcatgctgattgctccagccggtaaattcgagaaggggccgctggtgctttgcacgctggatgcttcc

gacggtgtggttttccgctggtttaacagcatgtatcacctgaccaccagctttctggaagaggcaccc

ttccagcagtatctgattcagcaaataccggtttccaggcgtcttgagacgctgcatgccatgcagtac

-continued

gaaaaggaagccaagcattggcgtccgccagaagtattcacccaactgacgctgctaccgatcccgtca

aggctgctgcgcccagtcgtgtttgtcagccagagcaaagacatttacgaggaaaatcacgagaccaag

atcaaccatctgatcaacgaagccaaacggcagatgagcctgtccaccggtacagggcaatcgggtcgg

ggcttcgatctgatcgcgagcattgcgattctgtttctgcctggcgcgatcatgatgcctgtctcgctg

ggcgctggcctttacaaaacctggagcgctttttcgaaaatcgatgaaaacgacctggaaggtgccgcc

gaggagtttctgagcgccctcagctatcttgccattaccttggtcggccatttggcgctggccttgaaa

ccggcaggaagcgccgcaaaaacggtgagacgtccgcacctggtacgcagagtcggtcgtgatgggcag

gcacagatcggctacctcctgtcgcattcaaaagcgccgcgtttcccagactcgaaattgatcgctgca

atggaccccaaacgcttcgtcgccattgaggtagaaggccagacctgcttaataagccggcgggccaac

ctgttcggccactcacgcctttatcgggtaaacccgatggatgcaacgcaactggtgcacgagcaggag

tttgccttgcgcagcaccaacggcacctggaaaatcgtgggcaaacagatcctgcgcatgagtcagtcc

gcaatccgcaatgcccaggctcaactgaccagcctgacaaatctctggccggcgtctctggaggaagca

agtagcgccgaacgcttgagcttcgagaccgactacctggcgctggcccagacatccaacgcagaaaac

tattccgaaatagtcgcctacgtggaaagcggttcaacagacatcaacccgctgctgcgaagcggcgtg

cgcaacgccaccacgcgcagatttttacgtcagttccataaactcaatgcgtgggaaggcactgccttt

cgcgccacctatgtgtccagcgacggggtggcatgccttgagcgcgaagtgggttcggtgttcaccgac

aacggcgtgcagtctgcatcggtgtcgcgagccaatgcctccagatggagccaggacgggttcgtgagc

agcaacgccaatgccgcaaaccacccggtgttcttcatctttgcaccgggagtgcccaagaagaacatg

ttcaccggctttcttggcgatcacgtggcaatcccgccaggcacgtgcgtgcaactgggtgcgaccaag

cggataaacggacagctgtttgcctggttcgatgcgcccgaacaaatggtcgatcagacctacgatctc

tatacaggagaacaggaactctgggtctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 88 as follows:

MTLTQRQAWHREAQRFGEQVVNMRKASKEHFGQAENDSRTYPARFIDQQLAQLLNRLSIAATAQQINIS

LTYRTGTEVLEIPGAPVLPETETENVSLRQLVHTQALRTKAKDAVLLRAVDAEGVPLAHLDKQAVTELI

ATLEDHRYLSDYLDLHLKTSAYAQQLKRSEKAMLQAQMKMALLEIEQQAFAPAGREWIKAVLDSPAPQG

RRTMAGESIEVRFFSVNQFKMTNVMLIAPAGKFEKGPLVLCTLDASDGVVFRWFNSMYHLTTSFLEEAP

FQQYLIQQIPVSRRLETLHAMQYEKEAKHWRPPEVFTQLTLLPIPSRLLRPVVFVSQSKDIYEENHETK

INHLINEAKRQMSLSTGTGQSGRGFDLIASIAILFLPGAIMMPVSLGAGLYKTWSAFSKIDENDLEGAA

EEFLSALSYLAITLVGHLALALKPAGSAAKTVRRPHLVRRVGRDGQAQIGYLLSHSKAPRFPDSKLIAA

MDPKRFVAIEVEGQTCLISRRANLFGHSRLYRVNPMDATQLVHEQEFALRSTNGTWKIVGKQILRMSQS

AIRNAQAQLTSLTNLWPASLEEASSAERLSFETDYLALAQTSNAENYSEIVAYVESGSTDINPLLRSGV

RNATTRRFLRQFHKLNAWEGTAFRATYVSSDGVACLEREVGSVFTDNGVQSASVSRANASRWSQDGFVS

SNANAANHPVFFIFAPGVPKKNMFTGFLGDHVAIPPGTCVQLGATKRINGQLFAWFDAPEQMVDQTYDL

YTGEQELWV

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-fifth nucleic acid molecule encodes ORF46 and has a nucleotide sequence according to SEQ ID NO: 89 as follows:

atgactcagctaaaccctgcgggacaaccgcccgcagaaccgacccgaatcgtcaaagctcacattgac

ctcatggatcctgccgaaagcgctgactacgaggcgacccgaatggcattgctcgcagcgatgcaaagc

ggcaatgccgcgatcaacctcgaacagattcggctcaagcccgacccagcgtccgggttcggcgaatac

tgcgctgagaaagctgcgctacctcacccggtccaggccgaaaaccaggaactcccgtttcagatagac

agcgatggcagcgtcagtctggcattgatgctgcgctataactacgggttgtcgctgccgcaatcgcct

gacgaaacagcgatcaaaaccctgctcaatacgctggcagaacttcgcaccagtcaagaactggggctt

attgatcagttcgacatcaaggccatgctgaccatgcaaaatctgcaggatctgaagcgagcctgcatt

gagtaccttggcaccgacggtggcacgctgctaggcaagctgggtgctgaaataattgcctcctgccca

gagtaccttggcaccgacggtggcacgctgctaggcaagctgggtgctgaaataattgcctcctgccca

ctggcagatgtgcagaactccccggtgacggttattgcccggattctcagatcggaaccggcaagggca

ttggggcaaacgctgctggcacagcttggtcggcctgaagaagaaacggacgcgtccctgacaacactc

gtggaccggattttatggtatgccatcagtagcgatcttcatgatccagaaaaccggaagccaggagaa

attgccggctatccattcacccaggccgaaaaccagggacgccgccacgctgacatcctgaacgatatt

cacaaccacctgatcaccacgggcaaggctgagtctgtcaacgaagcaataattgcctgcttcatactt

gcactcgatgactgcccggaatggctggtcagcagtgttcccgatgatctgccatacggctgtacagag

gtgtgggtcaactttcaacatggggtcacacttgcggaagtcatcgagtttggctcgtcacgctggatg

aactttgaagacctgatcgagctgccggtgattttcaacaaaaagatggacaccgaagagcagcaagtc

gcctatgtcgcaacgcgcatgcccattcttctgacttgggcccaggccaacggttacattcgtacccag

agcgacctgccttactccgaacaagagatagaacaggccgccagcgcgtttgaacactccgagaaacaa

tcccttgaagctgcgaacgccttgatccggaaagcgccagaacgcaaagccatggctatcagtgccatg

aaagaagcgcggaggacgcctgaaatagaaaaaatacttgagcaggaagattactggtttccgcccatc

gatctcggcatcaggctggcggtgctacgcaaaaatcacacgcctgtctatcgcgatcaccaaggcacg

ctctcaccgtcaaatctgccatacgacccctacggcataaaacacaaggcgtcgtcgttgctggagatc

tacatggcaggtgaaaacattgatgactggagactgccggggcgcaacagcaacgagggcctgcttccc

atcaaccgtgaaatgcagttgttgtacaaggcgctgccagacatcaatcaaaggttcgagagtgaatttt

caggcttatctggcagatgcccgtaaggcgtatgcgacgattatcagaaagttgctgactcacctgccg

ctcaagcaccgcatggcgatcgaaaatggtgaggtgtcgctacactcactcagattgccgaccaaggac

gtgctggcggcgacagagagcgaaaaacatcgggagccgttgcgagggcgcacgggctttgtcatcaaa

gctgtctacgagggcaaaaccacgttttacgaggtgtttccgttatcgatgattgtacgctatcgccct

gatctggaggcccttctcaagaacggtgtggtcggtatagatttttgggacattctgcctcccacccgt

ataccggtagcggtttataacggaatcacaatgccatttgatcagggagcctatttgaacggtcagcta

cctgagcctggggcaagcgctgtgatgattgcagaaaccattggtgaacgatttgattcttcaagtgca

gaggtcgggcaacaccagcctccgacctcgttttcaaaacgctctactggcattgccgagaccatcaca

acatcgcttttctacgtcaacgaagatgcactctttgcacactgcaaaagcctcacgcaggtagaaata

gataacggtgccccaggtgcgctcgaagaggtgtccagctttctgatacacctgacgccctggccggaa

atcgaaaacattctgtccggagagaaagcgcttatgaggggaggagcaatcggtctggcgctttacatg

attccctatgtgggacccgcgggcaagttgctcgcaggcacggcaaaagtcgttacccgcctgggcaaa

-continued

agcctcataaccagcggtagcaaagtccaggtctcgaaattgctcatcacggccggcaccaccctgaaa

gacgccccgctgatcatgatcagacaggcccctgacatgaccagtaaagcaatgactggcgtttcgcaa

ttcgtcgtgaaacacgtcacctggaaatttctggcgatacgtataggtattggtttaagccgcaggctt

gtagccatcatgagcaggcagcaggcccaggccgcaaagcaagaggccacgtaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 90 as follows:

MTQLNPAGQPPAEPTRIVKAHIDLMDPAESADYEATRMALLAAMQSGNAAINLEQIRLKPDPASGFGEY

CAEKAALPHPVQAENQELPFQIDSDGSVSLALMLRYNYGLSLPQSPDETAIKTLLNTLAELRTSQELGL

IDQFDIKAMLTMQNLQDLKRACIEYLGTDGGTLLGKLGAEIIASCPLADVQNSPVTVIARILRSEPARA

LGQTLLAQLGRPEEETDASLTTLVDRILWYAISSDLHDPENRKPGEIAGYPFTQAENQGRRHADILNDI

HNHLITTGKAESVNEAIIACFILALDDCPEWLVSSVPDDLPYGCTEVWVNFQHGVTLAEVIEFGSSRWM

NFEDLIELPVIFNKKMDTEEQQVAYVATRMPILLTWAQANGYIRTQSDLPYSEQEIEQAASAFEHSEKQ

SLEAANALIRKAPERKAMAISAMKEARRTPEIEKILEQEDYWFPPIDLGIRLAVLRKNHTPVYRDHQGT

LSPSNLPYDPYGIKHKASSLLEIYMAGENIDDWRLPGRNSNEGLLPINREMQLLYKALPDINQRFESEF

QAYLADARKAYATIIRKLLTHLPLKHRMAIENGEVSLHSLRLPTKDVLAATESEKHREPLRGRTGFVIK

AVYEGKTTFYEVFPLSMIVRYRPDLEALLKNGVVGIDFWDILPPTRIPVAVYNGITMPFDQGAYLNGQL

PEPGASAVMIAETIGERFDSSSAEVGQHQPPTSFSKRSTGIAETITTSLFYVNEDALFAHCKSLTQVEI

DNGAPGALEEVSSFLIHLTPWPEIENILSGEKALMRGGAIGLALYMIPYVGPAGKLLAGTAKVVTRLGK

SLITSGSKVQVSKLLITAGTTLKDAPLIMIRQAPDMTSKAMTGVSQFVVKHVTWKFLAIRIGIGLSRRL

VAIMSRQQAQAAKQEAT

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-sixth nucleic acid molecule encodes ORF47 and has a nucleotide sequence according to SEQ ID NO: 91 as follows:

atgtctgttacttcatctgtcctgcgactgtcgcgcctgagcgtgtcgttatcacttttgggcatgctg

tcgtctgcactgtttgccggcgcggcattcgccagcgacgagacgcaactgatcgaatccctcaacgcc

taccgtggccaggcgcagcgctgtggcgagcaggtgtccatggaactgccgccgctgagcaccgacccg

cgtctggtgctgcccgccagtggcaacctgaacctgcaacagtcgctgacccgcgcgtcttatcc9atg

gtcaccgtgcaggcgatcagtctgtccggaccgcgagatgcggcgtcggcgttgaaggcggtgcaggag

agtttctgccgcgtggtgctggacccgcagttcgtcgatatcggggtcagccgggacgggcgcgactgg

cgcatcgtgctggcgcgctcgctggtggcatcacgtctgggtgactggcaagcagaaggtcagaaaatt

ctggagatgatcaacaccgcccgtacccaggcgcgtcagtgcggttcgcaatccttcgcggccactaca

ccgttgagctggaatcaggtattggggacggccgcacaaggacactcgcaggcaatggccaatcagaac

ttctttgaccacaaggggcgcgacggccgcacgccgggtgacagggccgagcttgccggctatctgggc

cagcagatcggtgagaatattgccgcaggccaggacactgcccgcaaggtggtggacggctggctggtc

agcccgggccactgcgcaaacctgatgacccccggttttcgcgagctgggagccgcctacgcgatggac

cccaaaagtgacgcggggatttactggacagccatgttcggcacgcagcaatag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 92 as follows:

MSVTSSVLRLSRLSVSLSLLGMLSSALFAGAAFASDETQLIESLNAYRGQ
AQRCGEQVSMELPPLSTDPRLVLPASGNLNLQQSLTRASYPMVTVQAISL
SGPRDAASALKAVQESFCRVVLDPQFVDIGVSRDGRDWRIVLARSLVASR
LGDWQAFGQKILEMINTARTQARQCGSQSFAATTPLSWNQVLGTAAQGHS
QAMANQNFFDHKGRDGRTPGDRAELAGYLGQQIGENIAAGQDTARKVVDG
WLVSPGHCANLMTPGFRELGAAYAMDPKSDAGIYWTAMFGTQQ

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A forty-seventh nucleic acid molecule encodes ORF48 and has a nucleotide sequence according to SEQ ID NO: 93 as follows:

atgccgttattaaactggtccagacacatggttcatttaacagccatcggccttatcagcattccggct
gcctatgcagcggacaccctgacccgcgacaatggcgcagcggtcggcgacaaccagaactctcagact
gcaggcgcccaagggcctgtcctgctgcaagacgtacagctgctgcagaagctgcagcgttttgatcgc
gggcgtatcccggagcgtgtggtccacgcacgcggcactggcgtgaaaggcgaattcacagcgtccgcc
gacatcagcgacctgagcaaggcgaccgtcttcaaatcgggtgagaagaccccggtattcgtacgtttt
tcttccgtggtccacggcaaccactcgccagaaaccctgcgcggcccgcatggcttcgccaccaagttc
tacaccgctgatggcaactgggacctggtaggcaacaacttcccgacgttcttcatccgcgacgccatc
aagttcccggacatggtgcacgccttcaagcctgacccgcgtaccaacctggacaacgactcgcgccgc
ggcggcttcttctcgcatgtaccggaagccacgcgcacgctgaccctgctgtactccaacgaaggcaca
ccgaccggctatcgcttcatggacggcaacggcgttcacgcctacaaactggtcaacgccaaaggcgaa
gtgcactacgtcaagttccactggaagacgctgcaaggcatcaagaacctcgaccctaaagaagtcgct
gaggttcagtccaaggactacagccacctgaccaacgacctggtcggcgccatcaagaagggtgacttc
gcgaaatgggacctgtacatccaggtgctgaaacctgaagacctggccaagttcgacttcgacccgctg
gacgccaccaaaatctggcctgatgtgccagagaagaaaatcggccagatggtcctgaacaagaacgtc
gacaacttcttccaggaaaccgagcaggtcgccatggcacccgccaacctggtccctggtatcgagcct
tccgaagaccgtctgctgcaaggtcgagtgttctcctatgccgacacgcaaatgtatcgcctgggtgcc
gacagcggcaaaaccaccagcggcgtgaactacgagcctagccgtctggaaccccgtcctgccgatgag
aaagcacgttacagcgagctgccaatcagcggcactacccagcaggcgaagatcacgcgtgagcagaac
ttcaagcaggcgggtgatctgtatcgctcttacaacgcgaaagagcagaccgacctggtgcagagcttc
ggtgaatcgctggccgacactgacaccgaaagcaagaacatcatgctgtcgttcctctacaaggcagac
cccacctatggcactcgggtaaccgaagcggccaaaggcgatctggccaaggtcaagtcactggctgcc
agcctgaaagactga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 94 as follows:

MPLLNWSRHMVHLTAIGLISIPAAYAADTLTRDNGAAVGDNQNSQTAGAQ
GPVLLQDVQLLQKLQRFDRERIPERVVHARGTGVKGEFTASADISDLSKA

TVFKSGEKTPVFVRPSSVVHGNHSPETLRDPHGFATKFYTADGNWDLVGN
NFPTFFIRDAIKFPDMVHAFKPDPRTNLDNDSRRFDFFSHVPEATRTLTL
LYSNEGTPTGYRFMDGNGVHAYKLVNAKGEVHYVKFHWKTLQGIKNLDPK
EVAQVQSKDYSHLTNDLVGAIKKGDFPKWDLYIQVLKPEDLAKFDFDPLD
ATKIWPDVPEKKIGQMVLNKNVDNFFQETEQVAMAPANLVPGIEPSEDRL
LQGRVESYADTQMYRLGANGLSLPVNQPKVAVNNGNQDGAMNSGKTTSGV
NYEPSRLEPREADEKARYSELPISGTTQQAKITREQNFKQAGDLYRSYNA
KEQTDLVQSFGESLADTDTESKNIMLSFLYKADPTYGTRVTEAAKGDLAK
VKSLAASLKD.

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

This protein also has significant homology (e=0), as detected by BLAST search, to catalase isozyme catalytic subunit CatF from *Pseudomonas syringae* pv. *syringae* (GenBank Accession AAC61659, which is hereby incorporated by reference in its entirety).

A forty-eighth nucleic acid molecule encodes ORF49 and has a nucleotide sequence according to SEQ ID NO: 95 as follows:

atggggtttcgagctgcggcaaaagtgccgtcggtgcagaaatcgcccg

taacagcggcggtcgcctgatcgaaggcgatgcgttccatccccaggcca

acatcgacaagatgagcgccggcacccccctcaccgacgaagaccgtgcc

ggctggctgacccgtctgggtgaagaactggccgcagcccttgccaaggg

cgaacatccggtgctgacctgttcggcactcaagctcatttatcgtgaac

gcctgcgtgcggcggtgccgggcctgggttttgtctttctcgaactgagc

aaagagctggccaccgagcgttgcgccaaccggaccgggcatttcatgcc

tgcgagtctggtcgatagccagttcgcgaccctggaaccaccgatcggcg

agccactgaccctggtggtcgatgccagcaagcctatcgatgtaattggt

gaacaagccgcggcatggtggaaaggctctcacgcctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 96 as follows:

MGVSSCGKSAVGAETARNSGGRLIEGDAFHPQANIDKMSAGTPLTDEDRA

GWLTRLGEELAAALAKGEHPVLTCSALKLIYRERLRAAVPGLGFVFLELS

KELATERCANRTGHFMPASLVDSQFATLEPPIGEPLTLVVDASKPIDVIG

EQAAAWWKGSHA

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted. This protein also has significant homology (1.1e-52), as detected by BLAST search, to gluconokinase from *Pseudomonas aeruginosa* (Stover et al., *Nature* 406:959–964 (2000); GenBank Accession AAG05709, each of which is hereby incorporated by reference in its entirety).

A forty-ninth nucleic acid molecule encodes ORF50 and has a nucleotide sequence according to SEQ ID NO: 97 as follows:

atgcgaccggtgtctatgttttccctgcgttccatttgtgctgccgcactgtttgcgctttgcctgtct

atcttcccggcgctggccgccgagccgcccacccgcgatgccgtgcagcaaagcctcgacaagattgcc

gaccgcaagctgccggatgccgatcagaaggccttgcagcaggtgcttgagcagacgctggcgtttctc

aacagcaaagacgacagcgagcaaaagctgaccgcgctcaagcagcagctggctcaagcgccaaaacag

acctcggacaaccagcgcgagctggcccggttgaaagaaagcaaagtcgttgccgttgcacagcgctac

ggtggcctcgatgtgccgcaactggagcgactgctcagccagcgcagcacccagcaaagtgatctgcaa

agcgagcttaacgacgccaacagcctggccatcaccgcgcaaacccggccggagcgggcgcagactgaa

atcagcgccaatcagacacgcatccagcagatcaatgccatcctcaagaatggcaaagacaacggcaag

accctgagtgccgatcagcgcaatctgctcaatgcggaactggcctcgatcaacgcgctgaacctgctg

cgccgtcaggaactggccggcaacagccagttacaggacctgggcaacagccagcacgacttgctgacc

gaaaaagtcgcccgccaggagcaggaaattcaggacctgcaaaccctgatcaacgacaagcgccgagcc

cagtcgcagaaaaccgtggcggacctgtctctggaagcgcagaaatccggtggcagcagcctcctggcg

accgagagcgccgccaacctcaagctgtccgattacctgctgcgcggcaccgaccgtctcaacgagctg

acccagcaaaacctcaagaccaagcagcaactggacaacctgacgcagaccgatcaagccctcagcgag

cagatcaacgtgctgagcggcagcctgctgctgtccaagattctctacaagcaaaaacagtcgttgccg

cacctggaactggacaaaggcctggctgacgaaatcgccaacatccgcctttatcagttcgacatcaat

cagcaacgcgagcagatgagcacaccgaccgcttacgtcgaacgactgctcgccacccagcccccggaa

aatatcaccccgcaactgcgcaggacgctgcttgatctggccatcacccgcagcgacctgctcgaacgc

ctgaaccgcgagctgagcgcgttgctcaacgagtccatcacgctgcaattgaaccagaagcagttgacc

agtaccgccgtcggcctgcgctccacgctggacgagcagatgttctggatccccagcaacaagccgctg

gatctggagtggttccagaacatctggccgcgcctgcaaaaacaggtcgcgaccctgccctggacgtcc

agcctcagcgagctgtcggacggcttgacacaacgcccgctgctgtttctgccattgttactgctgatc

ggtgtactgacctggaggcgcaaggcgctttaccagaagctcaaccggctgcacgccgacatcggccac

ttcaaacgcgacagtcagtggaaaaccccgttggcgctgctgatcaacgtgctgctggccatgccggtc

gcattggggctggcgctgtgcggctacgccttgcaaatcgatgcgcgcgggcaaaacgccaaccttggc

-continued

gaggccttgctgcagatcgcgctggcctggctagtgttctacaccgcctaccgcgtgctggccccgtcc

ggcgttgcgcaactgcactttcgctgggaaccggcgcaggtcgcgttcttgcgcggctgggttcgtcgc

ctggggttggtggtgctggcgctggtcgccgtggtggcggtcgccgagcatcaaccggccgcgctggcc

gacgacgtgctgggtatcggcgtggtgctgacctgttacgcgctgatgacctggctgctgggccgattg

ctgctctccagccctacgcaccacaacgcgtcgctgttccgcaagacgctgggtgtggcgttcacggca

ttgccggtcgcgctgtttctggcggtgtgcttcggctactactacaccgcactcaagctcagcgaccgt

ctgatcgacacgctgtacctgatgatgatctggctgatggtcgaggccaccttcgttcgtggtctgggc

gttgccgcgcggcgactggcctaccagcgtgcgctggccaaacgtcaggctgcgcgagaaaacggtgac

agcgacatccccgtcgaagaaccgaaactggacatcgaacaggtcaaccagcagtcgctgcgcctgatt

cgtctggccttgctggctggtttcgtcggcgcgttgtacctggtctgggccgagctgatcacggtgttc

gcctacctggacaacatcatcctctacgaatacacaagcggcacaggcgccaacatgagcatggtgccg

atcagcctgagcgacttcctcggtgccggggtcatcatcgtcattacctttgtgctggcgggcaacctg

cccggcttgctcgagtgctggttctgtcacgcatgaacctggtcgcaaggcagcgcctatgcgaccacc

acgctgctctcctacaccatcgccggcatcggctttgtgaccacgctgtccacattaggcgtgagctgg

gacaagctgcagtggctggtcgcagcgctgtcggtgggcctggggttcggcatgcaggagatcttcgcc

aacttcatttccggcatcatgatcctcttcgagcgcccggtacggatcggcgacaccatcaccatcggc

gccctgtcgggtacggtcagcaagatccgcatccgcgccacgaccatcaccgacttcgaccgcaaggac

attatcgtcccgaacaagaccttcatcaccggccagctcatcaactggtcactgactgacaccgtcacc

cgcgtaacgctcaagctgggtgtggattacggctcggacctggacctcgtgcgctccctgctgctgcaa

gccgcacgggaaaaccctcgggtgctcaaggagccagagcccattgtctacttcctgaacttcggcgaa

agcaccctcgaccacgaactgcgcatgcacgttcgcgacctgggcgaccgcaacccggtactcgacgag

atcaaccgcttcatcaaccgcgagttcaagaaacagcacatcaacatctcgttccgccagatggagatc

tacctcaaaaacacccagggcctggaatacaaactggtgcccgccgaaccaggcgaaaagcacggcgca

ccggctgggcaaaccacgctgcaaccggtaaacaccaaagtagccccggcaaccaaagatgcgccagag

ccgccggagttgaggctggactga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 98 as follows:

MRPVSMFSLRSICAAALFALCLSIFPALAAEPPTRDAVQQSLDKIADRKLPDADQKALQQVLEQTLAFL

NSKDDSEQKLTALKQQLAQAPKQTSDNQRELARLKESKVVAVAQRYGGLDVPQLEQLLSQRSTQQSDLQ

SELNDANSLAITAQTRPERAQTEISANQTRIQQINAILKNGKDNGKTLSADQRNLLNAELASINALNLL

RRQELAGNSQLQDLGNSQHDLLTEKVARQEQEIQDLQTLINDKRRAQSQKTVADLSLEAQKSGGSSLLA

TESAANLKLSDYLLRGTDRLNELTQQNLKTKQQLDNLTQTDQALSEQINVLSGSLLLSKILYKQKQSLP

HLELDKGLADEIANIRLYQFDINQQREQMSTPTAYVERLLATQPPENITPQLRRTLLDLAITRSDLLER

LNRELSALLNESITLQLNQKQLTSTAVGLRSTLDEQMFWIPSNKPLDLEWPQNIWPRLQKQVATLPWTS

SLSELSDGLTQRPLLFLPLLLLIGVLTWRRKALYQKLNRLHADIGHFKRDSQWKTPLALLINVLLAMPV

ALGLALCGYALQIDARGQNANLGEALLQIALAWLVFYTAYRVLAPSGVAQLHFRWEPAQVAFLRGWVRR

LGLVVLALVAVVAVAEHQPAALADDVLGIGVVLTCYALMTWLLGRLLLSSPTHHNASLERKTLGVAFTA

LPVALFLAVCFGYYYTALKLSDRLIDTLYLMMIWLMVFGATFVRGLGVAARRLAYQRALAKRQGRENGD

-continued

SDIPVEEPKLDIEQVNQQSLRLIRLALLAGFVGALYLVWAELITVFAYLDNIILYEYTSGTGANMSMVP

ISLSDFLGAGVIIVITFVLAGNLPGLLEVLVLSRMNLAQGSAYATTTLLSYTIAGIGFVTTLSTLGVSW

DKLQWLVAALSVGLGFGMQEIFANFISGIMILFFRPVRIGDTITIGALSGTVSKIRIRATTITDFDRKD

IIVPNKTFITGQLINWSLTDTVTRVTLKLGVDYGSDLDLVRSLLLQAARENPRVLKEPEPIVYFLNFGE

STLDHELRMHVRDLGDRNPVLDEINRFINREFKKQHINISFRQMEIYLKNTQGLEYKLVPAEPGEKHGA

PAGQTTLQPVNTKVAPATKDAPRPPERLRD

The protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted. This protein also has significant homology (e=0), as detected by BLAST search, to putative potassium efflux system from *Yersinia pestis* (Parkhill et al., *Nature* 413:523–527 (2001); GenBank Accession No. NP_406604, each of which is hereby incorporated by reference in its entirety).

A fiftieth nucleic acid molecule encodes ORF51 and has a nucleotide sequence according to SEQ ID NO: 99 as follows:

atgtcaacgttgaatcatacgtctgctgtaaattgccgcgtcagttttgatggtgaccgttgctatgta

gacacccccdtccagatcatgccgggtgagcgatgggctgtaaatatcgtacctaacgatttagtcaca

atccactacgaggccgccagcaatcacgactacccttgctgctggccagcataaaaaatctgtttacc

gatgagcgttgtgtcgtgctaaagcccggccttacacagcaagctttgaacatgtatttttcagaggtt

aacagccttaaacctaacgcgactcatgttcgcttgttgcatcgagcgcagcgtatttttctagaaaac

atgatccgtagcgtacagataacctcgcaaggtatcagcgtcactttcgcaaccgccgaattcaaaaat

tataactaccagctaaaggtggataaatatacttttgcaaggcttgacaaggggtaccctctctattcg

gagctggttgaaaacacctggataacgaaattatccgtagcccataatattctgtattccatctctgtg

agcctggaccactcaagcacaccttatacacttttttcaggaaccctcgcggaagacaatatagtccag

ccgatacgggcgcttttcaccgacaacaccatgactcaactcacctccttggccgatcagaaaaccgtg

gatgccttgtatacgacggtcaatggcaacccggttatcagcatcaaaaaacgcgcagattatcggtct

tatctgaacatcgcacagaagttactgcttccaagaacctacaccaaagtagtacggacagtgagcagc

ctgtctgtgcattttacgggggaggcgtacaaacaattcaactacaagatgcttgtcaacaatgcttat

gcatccgagatcacccgagggaaggcttattactccagcgtgagcaatggggtgtggaccacttccggt

acgcatgacagcgacgacaactgcaaagtcacttgtgattacaagggcgcaacctacgtcctgtacgag

agtaatgcggcagatagacgcactgaaacctgggcacaagacccgtacgttactcattgcgacccgaga

gacctgtaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 100 as follows:

MSTLNHTSAVNCRVSFDGDRCYVDTPIQIMPGERWAVNIVPNDLVTIHYE

AASNHDYPLLLASIKNLFTDERCVVLKPGLTQQALNMYFSEVNSLKPNAT

HVRLLHRAQRIFLENMIRSVQITSQGISVTFATAEFKNYNYQLKVDKYTF

ARLDKGYPLYSELVENTWITKLSVAHNILYSISVSLDHSSTPYTLFSGTL

AEDNIVQPIRALFTDNTMTQLTSLADQKTVDALYTTVNGNPVISIKKRAD

YRSYLNIAQKLLLPRTYTKVVRTVSSLSVHFTGEAYKQFNYKMLVNNAYA

-continued

SEITRGKAYYSSVSNGVWTTSGTHDSDDNCKVTCDYKGATYVLYESNAAD

RRTETWAQDPYVTHCDPRDL

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-first nucleic acid molecule encodes ORF52 and has a nucleotide sequence according to SEQ ID NO: 101 as follows:

atgcgcctgatcgcgcagattctgcccggcctgccggaaaacaccacttacagcgccgccgctgcgtcc

aacaccctggcgcgggccatgcccaacgccattcgcaatgcgctgggcaccctggggctggtggctgcg

cgcacccagccaagcatctttccgttgccgtcgcgcaacgtcagcggtggcgaaaaagaggacgacctg

gagattctgctcaaactcgcggccgccgctgtttcgcgcctgcaaagccaccagttgggcggcctggag

cagacccgtaccaatgccgatggcactcaggtgactacatggcaactggaagtgccgatgcgcaacgcc

catgacatcgtgccgttgcaggtcaaggtgcagcgcgaagacaagcctgatcaggacgccaccgaagac

cgcgacgatatcgagatcaaggaaacccgtgaaaaactctggaaagtcgatctggctttcgacctggag

ccgcttggccccatgcaggtgcatgcgcaactgctgcgcggcacgctgtccagccagttatgggccgag

cgcccggatagcgcaacactgatcgaacatgaactggggcatttgcgcgagcgcgagcgccgattgccg

ctggccgtcggggaactggdgtgcagccatggcgttccgccgcaagggccgcgcaccgccctcgaacaa

cgctggatcgacgagaacgcctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 102 as follows:

MRLIAQILPGLPENTTYSAAAASNTLARAMPNAIRNALGTLGLVAARTQPSIFPLPSRNVSGGEKEDDL

EILLKLAAAAVSRLQSHQLGGLEQTRTNADGTQVTTWQLEVPMRNAHDIVPLQVKVQREDKPDQDATED

RDDIETKETREKLWKVDLAFDLEPLGPMQVHAQLLRGTLSSQLWAERPDSATLIEHELGHLRERLIACG

LAVGEIACSHGVPPQGPRTALEQRWIDENA

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-second nucleic acid molecule encodes ORF53 and has a nucleotide sequence according to SEQ ID NO: 103 as follows:

atgagtagcgtcgcagcactgatcaccatatcgactggacagacgcagttcgttaaagtcgcgcggacg

tcattttctgtgctacgaatccccctcgccggcagatgtcgtgtgtcgtgtccgggatcagttgaccac

aagacagagcagaaacccataaaaatagggggaagagacgtgagcctaaatgatcacttgaaaaaagca

ttgattctgatccagcgacgagcttgatgaaatcaccgacctttatgtgacgttgcctgcagaggtcga

ttcagttgcttgaccatttcactcgaagggaattggaaggaaattgatagcgtctggtctgctcggtta

gacgcagcagattcaaagaataatacaaaatgtcacgtccatatcgccaaaaaccaagcatcatcgatc

aaaagcaaacaggtttcttggaacagtgatggtagccggcatgataaaaaaaacattcgatgtgaacgct

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 104 as follows:

MSSVAALITISTGQTQFVKVARTSFSVLRIPLAGRCRVRDQLTTTIKTEQKPIKIGGRDVSLNDHLKKA

LNSDSSDELDEITDLYVTLPAEVFSCLTISLEGNWKEIDSVWSARLDAADSKNNTKCHVHIAKTKHRSS

KSKQVSWNSDGSRHDKKTFDVTLGQSRKAQAIARKFLGLGESISLESKDSKQMVERPLLSTATSFSNDG

KEVKVEFYVEESTAHLPAWLRW

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-third nucleic acid molecule encodes ORF54 and has a nucleotide sequence according to SEQ ID NO: 105 as follows:

atgaagccaatccatactgcccgatacaacgcctggaatcagttggagcaggagaccgcccatgactgg

ctgggggccaaaccccttggccagcagcacccttggctaccgctacgatgactggaaccagcgatgctgc

accacgaccgatgacaacgtacagacttatgagtattcagacccgatcggcagcgacgtacataaaggc

ccaatccagaaaacctggaaacagagtggcgacccggagggccgcatcagtggccgcagcgaaacctgg

ctgaatctgttcggcaaaccggaccggatccggacgctgaccgctggtaaaacgggtcgcagccgcacg

cacagcatgagccgcagccggaacctgaccacgactgagcaggaactgagcaggcagacctttctgtac

gacgggctgggacgctgcaccgagcagcgcgatgcactccagcaaagcaccctgttcagctacgacadc

tggtcacgcatggtctcctccacgcttgcagacggcagcgtcatcaaccggagttatgcgccgcaaagc

agcagtgagctggcaacgatgctcgaggtcgtgcaccagaacggcaccaccagaaccgtggcaggtaca

cagaaatttgacgggcttgagcgtgtgacgcagaccaaaacaggtgaccgcgtcgaacagttcaactac

gacgccggtgagatgcagcccaggtcgcgcacaacagccgggctggacaacatcaactttacctacact

cgggcgctcactgatcagatttttccagcacggctccggatgaaacggccaaattcgattatgacaag

accagtgcccgcctcatcgaagcgacgaacccgcaaggcacgcgcacttaccgctatgacgtgcacaat

caactgacgggagagacttgggacaatctgctgggtcaggcttgggaaacccgacaccaatcatcgctg

ctgggtcggccgatcaagcgcaccgatctcaaaaaaggcgaggcggcgggcgcagagacccgttacgac

tacgacacgctcggcagaatcaggtttatcaaccagagcaacctgcgcaccacaatcgactatgacgtg

ctgggccagctctgcaaggtggccaccgaggacctgcaggccggaactggcgtgatcatcgacatggaa

tacgacgaccagggacaggaaattctcagaacccagaccgcaagcaaccaagcggcgttgaccttgact

caaacgtgggcagtggacgggcttttgaaaacccgcgacctgcaacaggcgggtagccccctgctgcac

gaaacgtttagctacgaccccagaggccgcctgacactggtgaattacctgggtagcagcttgccgaga

gacgaactgcaaagggagatgaccagacaaatattcagcttcgacgagctggacaacattacgctatgc

cagaccaggtttaccgatggcacctctgagcgagcagctttcaaatacggcagccccggcgacgataag

cataaagaccgctgccagcttttgagtattgcctacacgccgcccagaaaaacaccggacccgacattc

agttacgacgccaacggtaaccagcttaaagacgagcatggcaacagtctgcattacgatagccagagc

cgcctgctgcaggtcgcagaaaccggcggtgcccctatcagccaataccgttatgacggccacaatcaa

ctggtcgccaccagggatggcaatgaaagcgagattttgcggttctatgagggtcatcaactgagcagc

acggtgcaggaagatcaacgcactcagtacctgcatctcggcgaacagccgctgggccagcagattgtg

gacgacgccgagcaaaccctgttgctactgactgacgcaaaccagagcgttatgggtgaatttcaacaa

-continued

ggccagctgcgcaaggcggtctacagtgcctacggggagcgccacagcgaggaggcgctgctgagcact

gccgggtttaacggtgaagtacgcgaagccgccaacggctggtatctgttgggcaatggctaccgggcc

tacaaccctctcctgatgcgcttccacagcccggattttctcagccccttcgccgaaggcggcgtcaac

ccctacacctactgcctgggcaaccccatcgccctgcgegacccgacaggacatgatgccagcggtcag

actggccggttgagacggcccgatgaggggggctttgccaatgcaacaaggtggcggagatatcatgggt

tgggtgggtgtaggaataggcgttgttttcaccgtattgggcgttgccgctaccatagccacgttagga

acagccacaccggttaccggcccggtaactgtcctgggcatttccatgaccgccagcgctgccgcggcc

gtttcgacagtctcgaccggtgcgttgatcgtcggtacggcattgacagcggcttcaactacggccaat

acagttgccattgtaaataacgatcagacggccggagaagtcggcggctggttgggtattgccgctgtg

cccgttggcttggtagggtttggcgcgggggctgtggtggcgagggcagttgcggctgcggctaaagtt

gcggctgccaacgctggtacgatcggtgtccgcagcgtcagcagaataggcctcgctgctgctggtgcc

cgcagaaccatttccagcgctgccagcagcgctcggcgccaaatcagcaacatgttaggcagaatctta

ccccgtgctctaaacaggactgctgctactgcacgccggattccaagcgttacaagtggcggatcagga

ccagggccatcattatttacacagaetacctttaacgaategattgggatgacgcagaecaetattttt

tcaacgaatgcgagcggaatcccaccggccacgcaggtaactcgaatctag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 106 as follows:

MKPTHTARYNAWNQLEQETAHDWLGAKPLASSTLGYRYDDWNQRCCTTTDDNVQTYEYSDPIGSDVHKG

PIQKTWKQSGDPEGRISGRSETWLNLFGKPDRIRTLTAGKTGRSRTHSMSRSRNLTTTEQELSRQTFLY

DGLGRCTEQRDALQQSTLFSYDNWSRMVSSTLADGSVTNRSYAPQSSSELATMLEVVHQNGTTRTVAGT

QKFDGLERVTQTKTGDRVEQFNYDAGFMQPRSRTTAGLDNINFTYTRALTDQIFSSTAPDETAKFDYDK

TSARLIEATNPQGTRTYRYDVHNQLTGETWDNLLGQAWETRHQSSLLGRPIKRTDLKKGEAAGAETRYD

YDTLGRIRFINQSNLRTTIDYDVLGQLcKVATEDLQAGTGVIIDMEYDDQGQEILRTQTASNQAALTLT

QTWAVDGLLKTRDLQQAGSPLLHETFSYDPRGRLTLVNYLGSSLPRDELQREMTRQIFSFDELDNITLC

QTRFTDGTSERKAFKYGSPGDDKHKDRCQLLSIAYTPPRKTPDPTFSYDANGNQLKDEHGNSLHYDSQS

RLLQVAETGGAPISQYRYDGHNQLVATRDGNESEILRFYEGHQLSSTVQEDQRTQYLHLGEQPLGQQIV

DDAEQTLLLLTDANQSVMGEFQQGQLRKAVYSAYGERHSEEALLSTAGFNGEVREAANGWYLLGNGYRA

YNPLLMRFHSPDFLSPFAEGGVNPYTYCLGNPIALRDPTGHDASGQTGRLRRPDEGALPMQQGGGDIMG

WVGVGIGVVFTVLGVAATIATLGTATPVTGPVTVLGISMTASAAAAVSTVSTGALIVGTALTAASTTAN

TVAIVNNDQTAGEVGGWLGIAAVPVGLVGFGAGAVVARAVAAAAKVAAANAGTIGVRSVSRIGLAAAGA

RRTISSAASSARRQISNMLGRILPRALNRTAATARRIPSVTSGGSGPGPSLFTQTTFNESIGMTQTTIF

STNASGIPPATQVTRI

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-fourth nucleic acid molecule encodes ORF55 and has a nucleotide sequence according to SEQ ID NO: 107 as follows:

atgcggtgtgtgaggcgatcaagaaggttctttaagctgcaagctgcaagctgcaagaaaaagcaggac

cgctttagcttagctgacgctccactgagtactttccatcgaacgatccgaaaaaccctgcctcgaaag

-continued

cttgtcagacccttttctgaatcagctatcgaggtagtcatgtccatcgaaccccaacgtcagaaagaa

cagccacccggccagcacacgccagcggatcagggcccggatcgcaatgatccggccatcgagccgcag

gtttcggacgtagagccggagactgaaaaaggtgacggccagacgcaaggccagacccctgcccccagc

caaagccagtcacaaagtcagaatcagagccagcagtccaacggcagcgcttacgtgcctgactatgag

ccgcaggaaaaaaaggaagaccagcgcaatcatcagcccactcaaggcactgatgctgatatcgacacc

aatgcgggctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ-ID NO: 108 as follows:

MRCVRRSRRFFKLQAASCKKKQDRFSLADAPLSTFHRTIRKTLPRKLVRPFSESAIEVVMSIEPQRQKE

QPPGQHTPADQGPDRNDPAIEPQVSDVEPETEKGDGQTQGQTPAPSQSQSQSQNQSQQSNGSAYVPDYE

PQEKKEDQRNHQPTQGTDADIDTNAG

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-fifth nucleic acid molecule encodes ORF56 and has a nucleotide sequence according to SEQ ID NO: 109 as follows:

atgcccgtcactggtgcaggctttatcaagcgtttgacgcaattgtccctctgcgccggcatggcgctg

gtcccggtggccgtacaggcagccgaaagcgatccttgggaaggcatcaaccgttccattttcagcttc

aacgataccttgacgcttatacgctcaagccgctggcaaagggttatcagtacatcgctccgcagttt

gtcgaagacggtattcataacttcttcagcaatatcggcgatgtcggcaatctggcgaacaacgtcttg

caggccaaacctgaagcggccggtgtagataccgcacgccttatcgtcaacactacgttcggtctgctg

ggcttcattgacgtcggcacccgcatgggcctgcaacgcagtgatgaagacttcggccagacactgggc

tactggggtgtgccaagcggcccgttcgtggtgattccgctgctgggcccaagcacggtgcgtgacgcc

attgccaagtacccggacacctacacctccccgtaccgctatattgatcacgtacccacccgcaacacg

gcgttgggcgtcaatctggtcgacacgcgtgccagcctgctgtccgccgagcgcctggtcagtggtgat

cgctacaccttcatccgcaacgcttacttgcagaaccgcgaattcaaggtcaaggacgggcaggtcgaa

gacgatttttaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 110 as follows:

MPVTGAGFIKRLTQLSLCAGMALVPVAVQAAESDPWEGINRSIFSFNDTLDAYTLKPLAKGYQYIAPQF

VEDGIHNFFSNIGDVGNLANNVLQAKPEAAGVDTARLIVNTTFGLLGFIDVGTRMGLQRSDEDFGQTLG

YWGVPSGPFVVIPLLGPSTVRDAIAKYPDTYTSPYRYIDHVPTRNTALGVNLVDTRASLLSAERLVSGD

RYTFIRNAYLQNRFFKVKDGQVEDDF

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-sixth nucleic acid molecule encodes ORF57 and has a nucleotide sequence according to SEQ ID NO: 111 as follows:

atgacactttcaaccctgcgccctaccccgcgccagcagtatgaatcgcccgagtcagccgaggatttc

acccagcggctggccgacctgacccgcacgctggccgaaacagccgagcagtacgacatcagcgcgcag

ttccctcacgccaacttccgcttgctgcacagccacggactgctcggcctgaccgtgcctgccgaactg

ggcggcggcgctgccgacctgtcgcgggcgcagcaggtcatcagcgcagtggccagaggcgagccttcg

acagcgctgattctggtcatgcagtacctgcagcattccaggctgcaggacaaccgcaactggccgagc

cacctgcgcgaacaggtggccaaagacgccgtgcacgagggcgcgctgatcaacgcgctgcgtgtcgaa

cccgacctgggcacacctgcgcgtggcggcttgccgggcaccatcgcccggcgcagcgccgaaggctgg

cgcatcagcggcagcaagatctactccaccggcagccatggcctgacctggttcgccgtgtgggcgcgc

agcgatgacgaggacccgctggtcggcagttggctggtgcacaaggacacgcccgggatcagcatcgtc

gaggactgggaccatctgggcatgcgcgccacctgcagccacgaggtcaggttcgacaacgtgcgagtg

ccgctcgaacacgcggtcagcgtcagtccgtggagcgccccgcaatccgagcttgatggtgccggcatg

ctgtggatgtcggtgctgctgtcgtcggtctacgatggcatcgctcaatctgcccgcgactggctggtg

cactggctggaacagcgcacgccttccaacctgggcgccgcgctgtcgaccctgccgcgctttcaggaa

acagtcgggcagatcgacacactgctgttcgccaaccgcagcctgctggagtccgccgcccaagggcac

acacccgcacagcatgccgcgcagatcaaatacctggtgaccggcaatgccatccgcgcagtggaactg

gccattgaggcctcgggcaatcccgggctttcacgcactaacccgctgcagcgtcattaccgcaacgtg

ctatgcggccgggtgcatacgccgcagaacgacgccgtgttgatgggcgtgggcaaagcggtatttgcg

gcacgcaagcagagccagtaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 112 as follows:

MTLSTLRPTPRQQYESPESAEDFTQRLADLTRTLAETAEQYDISAQFPHA

NFRLLHSHGLLGLTVPAELGGGAADLSRAQQVISAVARGEPSTALILVMQ

YLQHSRLQDNRNWPSHLREQVAKDAVHEGALINALRVEPDLGTPARGGLP

GTIARRSAEGWRISGSKIYSTGSHGLTWFAVWARSDDEDPLVGSWLVHKD

TPGISIVEDWDHLGMRATCSHEVRFDNVRVPLEHAVSVSPWSAPQSELDG

AGMLWMSVLLSSVYDGIAQSARDWLVHWLEQRTPSNLGAALSTLPRFQET

-continued

VGQIDTLLFANRSLLESAAQGHTPAQHAAQIKYLVTGNAIRAVELAIEAS

GNPGLSRTNPLQRHYRNVLCGRVHTPQNDAVLMGVGKAVFAARKQSQ

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-seventh nucleic acid molecule encodes ORF58 and has a nucleotide sequence according to SEQ ID NO: 113 as follows:

atgaatctcacaacacttcctcttgcgctcagcattgcttgcgctgcggccatcacacctgccttcgcg

ggcacaagcgtctctgaggcttcacacaaagtgaatgtgcagcaagttcgtaacgcgacggtaaagatc

tcctacggcggcacgacctttctgatcgacccgatgctggccaaaaagggaacctacccagggtttgaa

aatacctatcgaagcaatctgcgcaatccactggttgatctgaccgaatcgcccaccgaagtgatcgcc

ggtatcgacgcagttatcgtcactcatacgcaccttgaccattgggacgatgctgcacaaaaagtgctg

cctaaagacatccctctgttcacccagcatgaaaaagacgcgcagctgattcgctctcaaggtttcaag

aacgtacgcgtattgactgatgaagccgaattcggcggcgtcaaaattaccaagaccggtgggcagcat

ggcaccgacgaaatgtatgccgtgccagccctcgcgaagcctctgggtgaagcaatgggcgttgtattt

-continued

caagccccgggctacaagaccctctacctcgctggtgacactgtctggcgtaaagaggtcgatcaggct

atcgagaactattgtcccgaagtcatcgtactcaatgccggcaaagcaaaaatgacggggtatgagggg

gcgatcatcatgggggaagaggatgtactgcgcgcttcacaggtcgcgaagaacgcgaaaatcgtcgct

gtacacatgaatgcaatcaaccatatgtccctgacccgtgagcaattgcgcgcttacgtcaagcagcag

ggtatcgaaagtcgtgtagacataccggaagatggcgcttcactggagttctga

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 114 as follows:

MNLTTLPLALSIACAAAITPAFAGTSVSEASHKVNVQQVRNATVKISYG

GTTFLIDPMLAKKGTYPGFNTYRSNLRNPLVDLTESPTEVIAGIDAVIVT

HTHLDHWDDAAQKVLPKDIPLFTQHEKDAQLIRSQGFKNVRVLTDEAEFG

GVKITKTGGQHGTDEMYAVPALAKPLGEANGVVFQAPGYKTLYLAGDTVW

-continued

RKEVDQAIENYCPEVIVLNAGKAKMTGYEGAIIMGEEDVLRASQVAKNAK

IVAVHMNAINHMSLTREQLRAYVKQQGIESRVDIPEDGASLEF

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-eighth nucleic acid molecule encodes ORF59 and has a nucleotide sequence according to SEQ ID NO: 115 as follows:

atgcatctgttgccgtttgcgcgttacccctatcacctgcagaaacacctaaacccaaggtgaccatg

aaggttggagatttcagggcttacgacaccgctccagcacccggagtgaccactgcgtcctgcggacaa

ctggcaatcggcaccaagttagaaatcatcgagaccgccgagaatggcgaacttacttatgccaagggt

aagattctatctggcagcgtgaagcaggggcaaccaaaaaacgggtcgaggggcggaggtctggttc

gcttatttgaaaaacggcgaaccctacaaaaactcagtccctaagcgcatctggctcgctgacgatgtg

cctgagcgagcaagacccaattactggcagggtaaggtcaaagcctcagtagtgaataagttgccgctg

tacgatgatcctgccagccctacaaatggccagcctgcaggcgcccggaaggggactctggagctggtc

atgaacagcgtcatcgagtttaactcttcggaagtcgtcaacctggcgctggatggcaagctgcatcgg

atggccaagtgcacgatgctgagtggcggcctgcggggtcatggtgcggttccccccagcttttgggca

tgtgttgaaaatgaccctgctaataaagtattgaaatgggactcggtaacgccgaccagttttgatacg

gtcgttatgacgagcaccggagtgaaggcgggcgatccaattggctatcttggacaaaccgaaaatctc

accggtgaaaatggcggcgtcagcagcaaataccaggttcacgtcgaaattttcacagccgatgctgag

gttaaagacttcctcaagaacaccgcgggtttgaagattgggaagcaatacctgcaccttgcaagcggg

gctgtactcaagcaaaaagcgcccgcgaccggcaccacagcactcaagcaagaccatgcggttgacttg

gctaaagccacaattgtcaaagaaggcaccgatgactggtatgaggtcagcgtgatcgaggacgatcag

cctgtagccggcctgataaaaaaagccactgcgctagtcatcacacagcacgattgggaaaaattgggc

tttcagatcgtagaggagaacaacgcagcagccgatggtttcttggacccggatgcaatgccacagttc

ttcaaagacctattcgcgaagatcgacaagaaccacgatggtgaggtggagcctgctgaactggctgag

gctcttaagaaaccggaaaccagaacccagtgggccaggcttgttgcccatcaccctacggagtggaaa

gataaggcaggctcccccaagtggagcaagttggataaactgctggaaacgtcgccgaagatgttgaaa

catgaaaaagaacgcattgataaatatgtattttgggatgagttgtcagggaaagctaagatgacctca

agtttaatatggcattttcatccggtagaattcatttcaacatttagcgcaaaaaaagtctgcgcttgc

aacgccatagttaaggctactcgctgggtttcttccagtaagacgcactatggcccattgcatacgggt

gataaagagcttgggagtgcacctcagtgggatgacctggtctcagaaggaaaaataacggaagaggag

-continued

aaaaaaattattgttgtaatgtctggaaacgaggcaaaaattaacggagtacaaagttatgatagcgaa

ataattactgccggcgcgatgcdgaaaacaattaacttgtccggtggcggtgagctgccactacaagtt

aagaagtttaaaaatcagcatcccgaggcgtacatcgaatactttgattctcaaggctggaagttggat

gagacaggtgattcggcgaaaatgtattatcaagggccggctcgagctagtggcgcaaagctggaagga

aaggcgctgaaggataatttaaaaattggttgcagtgaatcgacatttgggaaggtggttgactgtcaa

cctgtttcagtgatggcctgcgctatcgcaagtccgttatatatccagatacaaataatggattttata

gaaaggttacgtagttctttaacgaagaagcccacaggctataactttactgctgggggatttttcaag

acctctctcggaaaagctgtggttttggatcacgatataaatcgacccgggtatgtgaaggatgacttg

ggatctgctcttgacacttttttttgctcaaaatccaacagtcagccgggatattgatacatggggcgca

gcatatagcgttaatgagcgaaaagttttagacctgtatggcgctcgaagaagaatgaccaatgcattg

cttcgatacaatcacttgaaggcggagttataa

20

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 116 as follows:

MHLLPFARYPLSPAETPKPKVTMKVGDFRAYDTAPAPGVTTAScGQLAIGTKLEIIETAENGELTYAKG

KILSGSVKQGATKKRVEGAEVWFAYLKNGEPYKNSVPKRIWLADDVPERARPNYWQGKVKASVVNKLPL

YDDPASPTNGQPAGARKGTLELVMNSVIEFNSSEVVNLALDGKLHRNAKCTMLSGGLRGHGAVPPSFWA

CVENDPANKVLKWDSVTPTSFDTVVMTSTGVKAGDPIGYLGQTENLTGENGGVSSKYQVHVEIFTADAE

VKDFLKNTAGLKIGKQYLHLASGAVLKQKAPATGTTALKQDHAVDLAKATIVKEGTDDWYEVSVIEDDQ

PVAGLIKKATALVITQHDWEKLGFQIVEENNAAADGFLDPDAMPQFFKDLFAKIDKNHDGEVEPAELAE

ALKKPETRTQWARLVAHHPTEWKDKAGSPKWSKLDKLLETSPKMLKHEKERIDKYVFWDELSGKAKMTS

SLIWHFHPVEFISTFSAKKVCACNATVKATRWVSSSKTHYGPLHTGDKELGSAPQWDDLVSEGKITEEE

KKIIVVMSGNEAKINGVQSYDSEIITAGAMQKTINLSGGGELPLQVKKFKNQHPEAYIEYFDSQGWKLD

ETGDSAKMYYQGPARASGAKLEGKALKDNLKIGCSESTFGKVVDCQPVSVMACAIASPLYIQIQIMDFI

ERLRSSLTKKPTGYNFTAGGFFKTSLGKAVVLDHDINRPGYVKDDLGSALDTFFAQNPTVSRDIDTWGA

AYSVNERKVLDLYGARRRMTNALLRYNHLKAEL

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A fifty-ninth nucleic acid molecule encodes ORF60 and has a nucleotide sequence according to SEQ ID NO: 117 as follows:

atgcggccgttgcctgcgttcagtattttgcagtttgatccgttgaaacgttcgggtcctgcgctgacg

gtcgaacgtgatacaccggtcgatagcaagcctattaatgacgtgcgttgtcgcttccgtacgtgctac

ccgaccgaagttcaggcgctggatctgaccgcgctgaattactcggtgaaaggcggtggttcgttgctc

agcctgcgcctggagatgagcgctgaaggtcacttgggtgagcttgaactgagccgcctgcgtctgcac

tttgcaggcgagcgctatatcagccagatgctgtacctctgcctgctacgcaatctcgagggtatcgag

ctgatccctctggacgctgccggcaagcccatcgacggtgtcaatggcgcgccaatggcgttcaagatg

ccgggcgaccgtgtacagccggtagggtttgccgaagaagaggcgttgatcccgtatccgctgaacacg

ttccgcggttatcgctacctgcaggagtacttcgcgtttcaggacaagttcctgttcgtcgacatcaac

ggtctggatctgctcaacgcactgccagaagagacactcaaacaagtgcgcggccttgagttgcgcttt

-continued

gatattegeaagageggeatteagegtcttegteeeaeeetggataaegtaaagetgtattgeaegeeg

atcgteaaettgtteaageaegaegeettgecgattegeettgatggeaageaggaegagtaeetgetg

etgeeegccgaatatggctggaaaeetgtggtgtgttteggttgaaaeegtgaceggttggaagecg

ggaggtettggetateaggattatgtgeegttegaateetttgageaegaeeeeagtttegaegtgeee

aaeagcegtcegeattacagcattegeeeagegttettetttgeteeatgaaggeetegaeaettatetg

agttteggeattegecataeagaagegeaegaaaeeetgtegategagttgatgtgeaeeaateagaae

ctgeeacgeaaactcaaaetgggegaaateaaegtggeetgegaagataegecggagtttttgagttte

egeaatateaeaeeeggetaeeteeagtttegegeeeeeegetgaaeegtgaetteetgtggaagttgate

agcaatatgtcgeteaattaettgtetetggetgacgteaatgcgetgaaggtgattctggaaaectae

gatttgcecegttaetaegaecageaegeggaaaaagteageaagegeetgttgggeggtttgaaateg

atcaageateaaeaegtggaeagattgeaeeegagggttaeeggtaegeggattgegeaetgagetgaee

atcgaeeeggaagggtatateggegaaggcgaeatgtttgtattegettcggtteteaaegagtttttte

gegetttaegeeagtctcaattegtaecaegagetgcgggtaaaaageaeacagggagaggtgtaeeaa

tggaeaeeaegtatgggeetceageeeetgetttaa

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 118 as follows:

MRPLPAFSILQFDPLKRSGPALTVERDTPVDSKPINDVRCRFRTCYPTEV

QALDLTALNYSVKGGGSLLSLRLEMSAEGHLGELELSRLRLHFAGERYIS

QMLYLCLLRNLEGIELIPLDAAGKPIDGVNGAPMAFKMPGDRVQBVGFAE

EEALIPYPLNTFRGYRYLQEYFAFQDKFLFVDINGLDLLNALPEETLKQV

RGLELRFDIRKSGIQRLRPTLDNVKLYCTPIVNLFKHDALPIRLDGKQDE

YLLLPAEYGLETCGVFSVETVTGWKPGGLGYQDYVPFESFEHDPSFDVPN

SRPHYSIRQRSSLLHEGLDTYLSFGIRHTEAHETLSIELMCTNQNLPRKL

-continued

KLGEINVACEDTPEFLSFRNITPAISSPAPPLNRDFLWKLISNMSLNYLS

LADVNALKVILETYDLPRYYDQHAEKVSKRLLGGLKSKHQIIVDRLHRGL

PVRGLRTELTIDPEGYIGEGDMPVFASVLNEFFALYASLNSYHELRVKST

QGEVYQWTPRMGLQPLL

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A sixtieth nucleic acid molecule encodes ORF61 and has a nucleotide sequence according to SEQ ID NO: 119 as follows:

atggtcaaggttacctcttccggatttactgccaaccctctctctcatcatgcggacagtgtttccccc

gcgaacagtccccctcagttaccggagcctgtgcatctggttgatttaagcgagtcgtcccgcaagggc

ggcatgcgaaatcggccgcatgccagtttgaacagtcaggtgctcgaactgcaagcggtgccgtcgcaa

cgtggaaagcatgttcgtgtcagaagtcatgccgatggcgagagtgtcattaatgcctggctggcaaag

cgcccctcggttcaaagcgaaaccagtcttgataacgatggcaaactggtgcgttacacccccgtgaat

catgagccgctggcgccgcgcaatgaggcgtttttcacctcggtgccggggatgttgatggccgttttg

acggtccaccccgagatggaacatggcatcagcggggacataactgctgatgctgtggctgcccggctt

gccgaaccgccaatagggttgctaaccggaatctggcagtcttcccatgatcgagcctatctggagcgt

ggcggtgtggtgcataccgccaatatggaagagcgctgggcgccgttgacgctgccaggcatcaatccc

cgagagcccctgcgaatggccggtttgcaggccgatggtggagtctatctgcataacggcagccaactg

tggcgcttgaccgaaactgccgccgagtccgtgaccaccgaaaaccttcctgaaggtgcggcggtacgc

attggcgccggtggcgaggtgcatgggctgcatgaaggcgcgcttcattcgaatggcatttcccgtcca

atcgagctttggcggccaaaagctggcgcgccggggcgcgagcagagtccggcgcgccccgttgatttg

-continued

ctgccgttaccgggtggcaccgctgcactgatccttgatgacaagggacgtatttatcacgctgatctg

aaaggcacaggcgctgttgaagcccaccggctgaaattacctgctgactttgcgcagggtaaaggttgg

gccgtgaccgccatgggattgtcccgagacgacactgttcatctgatgctgcaggatcagaacgggcgt

cgcatgagcttgcagcgagcaccgggcgaggcgctgtttcgtcctgcgtacctgctggatcgcccgttg

ctgctgctctataccgaagggctgcatgttccgtcggaggccgcggtgcagtcgcacgttcagcttgat

tgtcatgctcaactggggcatatcgatggcgtgctgcattataaagcggctcccgatcagtcatgggaa

gggctaaagcagtcgggcggcgaaccgctgacgggtttgactgctctttattccagcccgctgggattt

atcgacaggaaaccggttttcgctttagtgggggatgcccggcaggtggtcgagttgaaactggagggg

cgtacatcctggttgccgagcgatgccgagcttccgcgtcaccctgcgggcgggcctttggcggtgata

ccggatacggtagcgttacgcaccagcccgatcgcgcagtttgacgagcctgtacaggcgctggcggtt

cacggtaatcgccgggtcgtcgcgctgacggattcggggcgattaatggctgccgatgcggacacccca

gcccgccgacttcccacgttgcagcgccccatcgccatcgccgtagggctcaacgatcagttactggtg

ctgcatcatccccatagccagcgccccagttgaaacggttgagtgcgaaagatgactgggagccggtg

ccgataattctgccgggtattgttcacccttcaagtcttcgcgctactcgcacggggcaaatacaagtg

cagctgggagaaaactggcatacgttgctgccatcaatgacgtcgcacgataatcagcgcttacctgcc

cgcgtaaaacctgaaccagaggggatgaggcgccgtcggcgaatttcctggcgggtagcaacgccctc

gccaatcagcagcaagccagtcgtatcagcacaccgcatcatgacgcatcggtggttacgacgctggcg

gggacaacagccaacaacccgttgacgatggcgtcgagcctacaggcagtggttgatacgacccgcgct

caggtaggcgcgttggcgagagatgtagtgggcgcagcggcgaacagcacgatgcgggcdatggcgcat

accttgggtgttgtactgccgccaacgcctcaggagaagcgcctggccagtttccataatgaggcgaaa

caggcttatacatcaggaaaaatactgtttgagcatctgccgtcactcgcgcaagtgcgcgtcgcttca

gccgtagggccgtcggacggagaaagattcgggctgtcacatcagcaaacgcaacgcttgttgacgctg

cgagaggggaagctggaagcgctgttacgcgacttgcgcaagatcggctttcatgaaggggtgatcatg

ggcgatatgggcgacagcgacagtgcgcacggtcttgtttcgacgacatcgacaccaacgttccggctg

gccgagctatggcgacggcagcattcgcgagtggataaggcgctgtcttccgctggattatccagatcg

gaagatatttttccggacttgaacctaagtatcaacgcgttggctggcggcgcggcgctgaatgcggat

cgtatgagcgaacgtgaagctgagttgttgagcgttttgtgcgaggtcagcgaaaaaatgatgcgcgct

ggcgtacgcttgccggcagatgatggaagcgttgacagcgcccacagccaggcgccatacggcttgaga

acagcaggattgattgcaggtctggtggactatgatgcgctgttgagcdgtaccgacgcgcaggcgctg

gaaatggcggagcgacttcagcaagatgccaggcttgctgcattgtgcaaactcggtctgtcttcgtgg

ggtcaattagcggccttcgatgatgtggtgacgacgtttcgcgaacagatatcgttaccgggctcggca

cgccgcacccagttgctcaaaaatcttggcttgccacccgatgccgcgccggacgaaatggcggcgcgc

atgtccgacttactcctggatctgttcaaccggagcaccttcttttcgacgcagtcgcgtggtctggaa

ctgcgcggttcgttgggatcggctgactggaaacatctcaatgcgttcagcgtcggcgtgactggcgag

gcgcttcaagtgctcggcgtagagcgcatcggcgatggcaaggacggcgatgccgggttggtcgcgttt

tttgtgcgccacgccaaagcctctgtatctgcgacgtcagggatcggaatcgatttcaagccaggcccc

ggcactggcggccgtgttattgattcgcgaccgggtcgctcgatgaactcgacgtggggaggctctacc

aacctgggtatttccggcgcgtaccagcatggtcagggcgccgccgtgatcatcgcaccgtcgacgatc

tccgatttcgtgcggctgttattcgatgtcaaccatcccgataccacccaaatcctgcgcaccggtgtg

aacggtggttcgattggtcttgatctgtttgaaaccaatgtgaatgcctctgtgggggcgaacgtcagc

-continued

gtatcgccattcagcctgagccagaaatatgggccacagaaaccgacggcagatgcggccgtctctgac

ccagacaatcggcgcagcaccgcgtcagggtcgttgtcggtaggcgggacggctcaggctggcAcgcac

tgggggcaaatggagttgcacctggatcacgcctgggccgatattatcggtctggaatttcagggccgc

acggatttcaatcttgaattcaatagcggcctgaatctgggaggcgcgctgtcttccgcgctgggcgat

aacccccaaaagttgataaatgcgtccactggaaacggcaatctgcaactcgccggcatccgcgtcgcg

tcaagcgatgtgcagttgccgaccgatgctgtggttgacgacaagcgccgtggccccttcctgtcgacg

gccagctataaacgcaccttcgataccgaagttgccaagcctgttacggccggggagtggagccagatg

cgccagcgccttgccaaagcctttcctgacaatatcgcagagttgggcgcgctcgattaccccaccagg

cccggtgagcgtatcgcgaccatcaaacaggtgattgaccgcatacaaggtgcgaaggcgcgtagcgtg

gaagccgtcggtgcaatggacggaaaggcattgcaccgtcagcgtttcgatgccgcgagagaaatgtcg

aacgccggcaacagcgtatggcgggcgagttccgaaattgagcgcgcctcgatcgtggagatgctgcat

cagttgcgtcagcaggaacaaagcgccgtccagaatcacgcccgagccattcccggcgcgcgtgtggaa

ttcaacctgttcggtcgtgaatcgctggaaacggtggtctttcacgccatcggtcatctggggcttggc

agcaagctgaacgatctggcggagctgcgtcgcaaggtgccgggtctcgatcaggtcatgctgagtttc

cagtcgttgcccaaggtcaatcaggtgcgctacgtttttgagatgcgccctcaggcgaggttcgccatc

aatgacgcgctactggcgcgcgagcagcaggcatcggcacgtgcgctcggtttgcagggaccctcggga

agtgaattgaattggcgcggcgttctggacaagatcaaaaccacgcctgacctttatcggctggcggcg

atcgccgtacataacaccgatgaaaaccccgtgacctcaagaatagggctgecgetgctgaatgtgtcg

gccacaggcgcgacatcgcatcagttgttcgaggcggaaatccagttccgatacggtctgtatgacggt

ctgcaaggggttgagttgctggaggccggaaacagggcattgcagtcgccgttacgggcattacagcaa

tccggtattcaggccctggggcagagaacccaggccggggaggttgcgtatggcccccttcgccgcgc

aaagagtcgccgttgcgcaccgcagtggatgctgctgcgctgacaacgagtgacatcgcgcgacaactt

gaggttaaagtccagcgcatgaataccgcgcatgagcgtgaggcgaatgctatcagttcgttccagcag

gcttatgggatcgcgtccgcgcatctagacaggctgcttttgcgcattcctgaattgccattacctgaa

attgatgaccgcgacgtcgatggaggacgtgtgcgcggtacatttgcgtcgctccagcgacatcatcag

gcgctggatgacgctataagtgccatgcatcaggccagcgaaaaggtgtacacgatacctggcaagcag

gccactcaagagcaagacccggcgctggctcaactgctctctgttgaaaaacgtcggcgttcgctcggg

catgccttggaaacactggcgggcagaggggtggaagcgggcacggccacagggcttgaacttaacagg

gtctcatcgcaagtgaatgatctggtcgctcgccgggacgcgctgctaaggcagcgtgaaagcggtgtt

caggagggcggtctggatagcgaagagctggaaatggaacttcaattgaccacctcagtgctgcagcgg

ttgcgcgccgatttgctcggcgagcggcaggcgatggaggctaccgccaaacgcctggatcaggcgagc

cgcgctgccctcgaaggtgagcgcagcttcagcgacgccgtgcgtgacagggcgtggggcgaactcgat

aacgtgtag

The protein encoded by this nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 120 as follows:

MVKVTSSGFTANPLSHHADSVSPANSPPQLPEPVHLVDLSESSRKGGMRNRPHASLNSQVLELQAVPSQ

RGKHVRVRSHADGESVINAWLAKRPSVQSETSLDNDGKLVRYTPVNHEPLAPRNEAFFTSVPGMLMAVL

TVHPEMEHGISGDITADAVAARLAEPPIGLLTGIWQSSHDRAYLERGGVVHTANMEERWAPLTLPGINP

-continued

REPLRMAGLQADGGVYLHNGSQLWRLTETAAESVTTENLPEGAAVRIGAGGEVHGLHEGALHSNGISRP

IELWRPKAGAPGREQSPARPVDLLPLPGGTAALILDDKGRIYHADLKGTGAVEAHRLKLPADFAQGKGW

AVTAMGLSRDDTVHLMLQDQNGRRMSLQRAPGEALFRPAYLLDRPLLLLYTEGLHVPSEAAVQSHVQLD

GHAQLGHIDGVLHYKAAPDQSWERLKQSGGEPLTGLTALYSSPLGFIDRKPVFALVGDARQVVELKLEG

RTSWLPSDAELPRHPAGGPLAVIPDTVALRTSPIAQFDEPVQALAVHGNRRVVALTDSGRLMAADADTP

ARRLPTLQRPIAIAVGLNDQLLVLHHPHSQRPQLKRLSAKDDWEPVPIILPGIVHPSSLRATRTGQIQV

QLGENWHTLLPSMTSHDNQRLPARVKPEPEGDEAPSANFLAGSNALANQQQASRISTPHHDASVVTTLA

GTTANNPLTMASSLQAVVDTTRAQVGALARDVVGAAANSTMPAMAHTLGVVLPPTPQEKRLASFHNEAK

QAYTSGKILFEHLPSLAQVRVASAVGPSDGERFGLSHQQTQRLLTLREGKLEALLRDLRKIGFHEGVIM

GDMGDSDSAHGLVSTTSTPTFRLAELWRRQHSRVDKALSSAGLSRSEDIPPDLNLSINALAGGAALNAD

RMSEREAELLSVLCEVSEKMMRAGVRLPADDGSVDSAHSQAPYGLRTAGLIAGLVDYDALLSSTDAQAL

EMAERLQQDARLAALCKLGLSSWGQLAAFDDVVTTFREQISLPGSARRTQLLKNLGLPPDAAPDEMAAR

MSDLLLDLFNRSTFFSTQSRGLELRGSLGSADWKHLNAFSVGVTGEALQVLGVERIGDGKDGDAGLVAF

FVRHAKASVSATSGIGIDFKPGPGTGGRVIDSRPGRSMNSTWGGSTNLGISGAYQHGQGAAVIIAPSTI

SDFVRLLFDVNHPDTTQILRTGVNGGSIGLDLFETNVNASVGANVSVSPFSLSQKYGPQKPTADAAVSG

PDNRRSTASGSLSVGGTAQAGAHWGQMELHLDHAWADIIGLEFQGRTDPNLEFNSGLNLGGALSSALGD

NPQKLINASTGNGNLQLAGIRVASSDVQLPTDAVVDDKRRGPFLSTASYKRTFDTEVAKPVTAGEWSQM

RQRLAKAFPDNIAELGALDYPTRPGERIATIKQVIDRIQGAKARSVEAVGAMDGKALHRQRFDAAREMS

NAGNSVWRASSEIERASIVEMLHQLRQQEQSAVQNHARAIPGARVEFNLFGRESLETVVFHAIGHLGLG

SKLNDLAELRRKVPGLDQVMLSFQSLPKVNQVRYVFEMRPQARFAINDALLAREQQASARALGLQGPSG

SELNWRGVLDKIKTTPDLYRLAAIAVHNTDENPVTSRIGLPLLNVSATGATSHQLFEAEIQFRYGLYDG

LQGVELLEAGNRALQSPLRALQQSGIQALGQRTQAGEVAYGPPSPRKESPLRTAVDAAALTTSDIARQL

EVKVQRMNTAHEREANAISSFQQAYGIASAHLDRLLLRIPELPLPEIDDRDVDGGRVRGTFASLQRHHQ

ALDDAISAMHQASEKVYTIPGKQATQEQDPALAQLLSVEKRRRSLGHALETLAGRGVEAGTATGLELNR

VSSQVNDLVARRDALLRQRESGVQEGGLDSEELEMELQLTTSVLQRLRADLLGERQAMEATAKRLDQAS

RAALEGERSFSDAVRDRAWGELDNV

45

This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A sixty-first nucleic acid molecule encodes a HrpA-related protein and has a nucleotide sequence according to SEQ ID NO: 121 as follows:

atgaacattacgccgctcacgtcagccgcgggcaagggctcgtccgcacaaggcacagacaaaatttcc

attcccaactccacgcgcatgatcaatgccgcttcaatcaagtggttgaataaggtgcgtagcgccatc

agtgaccacatccgcaccagcatcgagaaagggaaactgttcgagctcgcctccttgggcagcaacatg

ttcggtgtcccggctctttcagcgcgcccctcgacgctccaacctgtgttggcgtttgaggctgacccc

aatcacgacctgaaccttgtcagggtctatatgcaggacagcgccggcaagctcactccctgggacccg

acgcccaacgcggtcacgacgacgtcgaatccatcagagcctgatgcgcagagcgataccggcttcgtca

tcattacctcggcggcctcccgcaggctcggtgctgagtttgctgggcattgcgctggatcacgcgcaa

cgccacagtcctcgcgcggacaggtctgccaagggacgacctggccgagaggagaggaacggggcaagg

ttcaatgccaagcaaacaaagccgacagaggctgaagcctacggtgatcatcagacacccaatcctgat

-continued

ttgcacaggcaaaaagagacagctcaacgcgttgctgaaagcatcaacagcatgcgagagcagcaaaat

ggaatgcaacgcgccgaagggcttctcagagccaaagaagcgttgcaagctcgggaagccgcgcgcaag

cagcttctggacgtgctcgaggccatccaggctggccgtgaagactccaccgacaagaagatcagcgcc

actgaaaagaacgccacgggcatcaactaccagtga

The Hrp-A related protein has an amino acid sequence according to SEQ ID NO: 122 as follows:

MNITPLTSAAGKGSSAQGTDKISIPNSTRMINAASIKWLNKVRSAISDHIRTSIEKGKLFELASLGSNM

FGVPALSARPSTLQPVLAFEADPNHDLNLVRVYMQDSAGKLTPWDPTPNAVTTTSNPSEPDAQSDTASS

SLPRRPPAGSVLSLLGIALDHAQRHSPRADRSAKGRPGREERNGARFNAKQTKPTEAEAYGDHQTPNPD

LHRQKETAQRVAESINSMREQQNGMQRAEGLLRAKEALQAREAARKQLLDVLEAIQAGREDSTDKKISA

TEKNATGINYQ

The HrpA-related protein, has significant homology, as detected by BLAST analysis (5e-07), to the C-terminal 43 amino acids of HrpA (GenBank Accession AF232004; Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856–4861 (2000), each of which is hereby incorporated by reference in its entirety). Expression of the hrpA-related gene is activated by HrpL, as indicated by miniTn5gus mutagenesis. This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted. HrpA is the Hrp pilus subunit protein (Roine et al., *Proc. Natl. Acad. Sci. USA* 94:3459–3464 (1997), which is hereby incorporated by reference in its entirety).

A sixty-second nucleic acid encodes ORF01152 and has a nucleotide sequence according to SEQ ID NO: 123 as follows:

atgaccttaagaatcaatactcgttctgctaccccggttgtacctctggaaacaggctctacatcgcag

ccgacaccaccgccggtcacggcaagagcgactgagcctccccccgtcgccaatcctgcggcgcctaaa

tcagcgccaggtgttcagcaagcacacgggctgaagacgcgcatcgctggcaagctttccgaacgtcag

accaatttcagtctcgggattcccggcactggtcgtactctcaaccggcccttgcgcagcgggattccg

gaggaaggtgagcaggtatcgaacgaggagagtcatgatccgttgctcaaggaagcgcatgaactgcag

cgtatggtggagtcggcgctgacccatctgaaggcggcaccgacgtctctctgggagcgtcccgcccct

tcaacggtaaggcgtattaccaccaagatttttccgtggctaaagcctgccccgctgcgcgaagtcgca

agcaatggcagcaacgccaagaccaagatcaagatcaactcacagcaaagccctgaaaccatcgcagcg

gcggtgaaagagctgagcacccggctcgatcaccagagcaaggtgctcgccacagccacccacgcactg

gtcgctgcgcgtgagcatcttgaatcgctcgaacaggccaccccgccctcgtcgaccgaaccactggac

catgccagggctcgcgttcaacaagccgactccaccacccgcctggccagtcagcaacttcgtgagctg

attcagggtacagacgtgttgcaactgggcgcgctgagtgaagggcaggatcaggttgaacagaaagcc

gagttttct

The protein encoded by the nucleic acid molecule has an amino acid sequence according to SEQ ID NO: 124 as follows:

MTLRINTRSATPVVPLETGSTSQPTPPPVTARATEPPPVANPAAPKSAPGVQQAHGLKTRIAGKLSERQ

TNFSLGIPGTGRTLNRPLRSGIPEEGEQVSNEESHDPLLKEAHELQRMVESALTHLKAAPTSLWERPAP

STVRRITTKIFPWLKPAPLREVASNGSNAKTKIKINSQQSPETIAAAVKELSTRLDHQSKVLATATHAL

-continued

VAAREHLESLEQATPPSSTEPLDHARARVQQADSTTRLASQQLRELIQGTDVLQLGALSEGQDQVEQKA

EFS

Expression of ORF01152 is activated by HrpL, as indicated by miniTn5gus mutagenesis (Fouts et al., *Proc. Natl. Acad. Sci. USA* 99(4):2275–2280 (2001), which is hereby incorporated by reference in its entirety). This protein possesses N-terminal Hop features (see U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, which is hereby incorporated by reference in its entirety), suggesting that it is likely to be secreted.

A sixty-third nucleic acid molecule encodes HopPtoF (formerly AvrPphF$_{Pto}$ ORF2) and has a nucleotide sequence according to SEQ ID NO: 125 as follows:

ataggtaatatttgcggcacctcgggctcacgtcatgtgtatagcccatcccatacacaacgaataact

tcagctccctctacatccactcatgttggtggagatacactgacatccattcatcagctttcgcatagt

cagagagagcagtttctgaacatgcatgatccaatgagagtaatgggacttgaccatgataccgagctt

ttcagaacgacggatagtcgctatataaaaaacgataaactcgcgggcaatccacaatccatggcgagt

atccttatgcatgaagaactgcgccccaatcgttttgccagccatacaggtgcccaaccacacgaagca

agggcgtacgttccgaaaagaataaaagccaccgatctaggagttccatcactgaacgtaatgactggc

tcgctagcgcgagacggaattagagcttatgatcacatgagtgataatcaggtctctgtcaaaatgcga

ctgggagattttctcgaaaggggtggcaaggtctatgccgacgcttcgtctgtagctgacgatggggaa

acatcacaagctctgattgtcacattgcccaaaggacagaaagtgccggtcgaaagggtctga

HopPtoF has an amino acid sequence according to SEQ ID NO: 126 as follows:

MGNICGTSGSRHVYSPSHTQRITSAPSTSTHVGGDTLTSIHQLSHSQREQ

FLNMHDPMRVMGLDHDTELFRTTDSRYIKNDKLAGNPQSMASILMHEELR

PNRFASHTGAQPHEARAYVPKRIKATDLGVPSLNVMTGSLARDGIRAYDH

MSDNQVSVKMRLGDFLERGGKVYADASSVADDGETSQALIVTLPKGQKVP

VERV

Contrary to the previously identified sequence of hopPtoF (see U.S. patent application Ser. No. 10/114,828 to Collmer et al., filed Apr. 2, 2002, which is hereby incorporated by reference in its entirety), hopPtoF possesses a rare ATA start codon, which is believed to be involved in regulating protein synthesis in DC3000. HopPtoF has been shown to be expressed by DC3000 and it has been shown to be translocated in planta, where it is localized to the plant plasma membrane and has a role in virulence. HopPtoF has also been shown to cause a hypersensitive response in *Arabidopsis* Col-0. The homologous *Pseudomonas syringae* pv. *phaseolicola* AvrPpbF effector protein has been shown to play a role in both development of the hypersensitive response and virulence in several plants (Tsiamis et al., "Cultivar-specific avirulence and virulence functions assigned to avrPphF in *Pseudomonas syringae* pv. *phaseolicola*, the cause of bean halo-blight disease," *EMBO J.* 19(13):3204–3214 (2000), which is hereby incorporated by reference in its entirety). Finally, HopPtoF has since been shown to be cytotoxic to eukaryotic cells, specifically cultured mammalian CHO and HEK293 cell lines.

A sixty-fourth nucleic acid molecule encodes IaaL$_{Pto}$ and has a nucleic acid sequence according to SEQ ID NO: 208 as follows:

atgactgcctacgatgtagaaaaggaatggagcagaatttccaatactgccgctaaaactcaccagaac

aacgattttgaaggtttcacctaccaggacttcagaacccacgtaccgatcatggacaaggaaggcttc

gcggcacaaaccgaacgctgccttgagcgcaacgagcgcaactgcctgatcggctttaccagtggcacc

agcggcaacctcaaacgctgttattactactacgactgtgaagtcgatgaagacagttcccgctccaac

gtcttccgcagcaatggtttcattcaacccggtgatcgctgcgccaacctgttcaccatcaacctgttt

tctgccctgaacaacatcaccaccatgatggccggtaactgcggtgcgcatgtggtgtccgtaggcgat

-continued

atcaccctgctgaccaagagtcacttcgaggcgctcaactcgatcaagctcaacgtactgctcggcgta

ccctcgaccatcctgcagttcatcgatgccatgcagcagcacggtgtgcacatcgatatcgaaaaggtc

gtcttcaatggcgagggcctgaaaaccttcagaagaaaatcatcagggaagcctttggcgaacaggtc

tccatcgtcggcgtatatggcagttccgagggcggcattctgggtttcaccaacagcccttgccacacc

gaatacgagtttctttccgacaaatacttcatcgagaaagaaggcgacagcatcctcatcacctcgttg

acccgcgagaacttcacaccgctgctccggtatcgcctgggagacaccgcaacgctttcgctgaaaggc

gacaagctctatttgactgacatccagcgggaggacatgagcttcaacttcatgggcaacctcattggt

ctgggcatcattcaacaagcgatcaaacagacactgggccgcacgctggaaatccaggttcacctgtca

gtgactgatgcgcgcaaagaactggtgaccgttttcgttcaggcctcggaagtcaacgaagatgaacgc

gccagaatcgaaacagccatcgccgatattccggacatcaacgaggcctatcagaaagaccagggcagc

gtgctggttgtgcgcaaggatgccagagactacgccgtctcggagcgaggcaaaatgctctacatcatt

gaccgcaggaat

IaaL$_{Pto}$ has an amino acid sequence according to SEQ ID NO: 209 as follows:

MTAYDVEKEWSRISNTAAKTHQNNDFEGFTYQDFRTHVPIMDKEGFAAQTERCLERNERNCLIGFTSGT

SGNLKRCYYYYDCEVDEDSSRSNVFRSNGFIQPGDRCANLFTINLFSALNNITTMMAGNCGAHVVSVGD

ITLLTKSHFEALNSIKLNVLLGVPSTILQFIDAMQQHGVHIDIEKVVFNGEGLKTFQKKIIREAFGEQV

SIVGVYGSSEGGILGFTNSPCHTEYEFLSDKYFIEKEGDSILITSLTRENFTPLLRYRLGDTATLSLKG

DKLYLTDIQREDMSFNFMGNLIGLGIIQQAIKQTLGRTLEIQVHLSVTDARKELVTVFVQASEVNEDER

ARIETAIADIPDINEAYQKDQGSVLVVRKDARDYAVSERGKMLYIIDRRN

IaaL$_{Pto}$ has significant homology, as detected by BLAST analysis (0), to IAA-lysine synthetase (GenBank accession M35373; Roberto et al., *Proc. Natl. Acad. Sci. USA* 87: 5797–5801 (1990), each of which is hereby incorporated by reference in its entirety).

Fragments of the above-identified proteins or polypeptides as well as fragments of full length proteins can also be used according to the present invention.

Suitable fragments can be produced by several means. Subclones of the gene encoding a known protein can be produced using conventional molecular genetic manipulation for subcloning gene fragments, such as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Laboratory, Cold Springs Harbor, N.Y. (1989), and Ausubel et al. (ed.), *Current Protocols in Molecular Biology*, John Wiley & Sons (New York, N.Y.) (1999 and preceding editions), each of which is hereby incorporated by reference in its entirety. The subclones then are expressed in vitro or in vivo in bacterial cells to yield a smaller protein or polypeptide that can be tested for activity, e.g., as a product required for pathogen virulence.

In another approach, based on knowledge of the primary structure of the protein, fragments of the protein-coding gene may be synthesized using the PCR technique together with specific sets of primers chosen to represent particular portions of the protein. Erlich, H. A., et al., "Recent Advances in the Polymerase Chain Reaction," *Science* 252: 1643–51 (1991), which is hereby incorporated by reference. These can then be cloned into an appropriate vector for expression of a truncated protein or polypeptide from bacterial cells as described above.

As an alternative, fragments of a protein can be produced by digestion of a full-length protein with proteolytic enzymes like chymotrypsin or *Staphylococcus* proteinase A, or trypsin. Different proteolytic enzymes are likely to cleave different proteins at different sites based on the amino acid sequence of the particular protein. Some of the fragments that result from proteolysis may be active virulence proteins or polypeptides.

Chemical synthesis can also be used to make suitable fragments. Such a synthesis is carried out using known amino acid sequences for the polyppetide being produced. Alternatively, subjecting a full length protein to high temperatures and pressures will produce fragments. These fragments can then be separated by conventional procedures (e.g., chromatography, SDS-PAGE).

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification, or identification of the polypeptide.

The proteins or polypeptides used in accordance with the present invention are preferably produced in purified form (preferably at least about 80%, more preferably 90%, pure)

by conventional techniques. Typically, the protein or polypeptide of the present invention is secreted into the growth medium of recombinant host cells (discussed infra). Alternatively, the protein or polypeptide of the present invention is produced but not secreted into growth medium. In such cases, to isolate the protein, the host cell (e.g., *E. coli*) carrying a recombinant plasmid is propagated, lysed by sonication, heat, or chemical treatment, and the homogenate is centrifuged to remove bacterial debris. The supernatant is then subjected to sequential ammonium sulfate precipitation. The fraction containing the protein or polypeptide of interest is subjected to gel filtration in an appropriately sized dextran or polyacrylamide column to separate the proteins. If necessary, the protein fraction may be further purified by HPLC.

Other DNA molecules encoding other effector proteins or polypeptides can also be identified by determining whether such DNA molecules hybridize under stringent conditions to a nucleic acid molecule as identified above. An example of suitable stringency conditions is when hybridization is carried out for about 8 to about 20 hours at a temperature of about 37° C. using a hybridization medium that includes 0.9× sodium citrate ("SSC") buffer, followed by washing for about 5 minutes to about 1 hour with 0.2×SSC buffer at 37° C. Higher stringency can readily be attained by increasing the temperature for either hybridization or washing conditions or increasing the sodium concentration of the hybridization or wash medium. Nonspecific binding may also be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein-containing solutions, addition of heterologous RNA, DNA, and SDS to the hybridization buffer, and treatment with RNase. Wash conditions are typically performed at or below stringency. Exemplary high stringency conditions include carrying out hybridization at a temperature of about 42° C. up to and including about 65° C. (inclusive of all temperature in such range) for about 8 up to about 20 hours in a hybridization medium containing 1M NaCl, 50 mM Tris-HCl, pH 7.4, 10 mM EDTA, 0.1% sodium dodecyl sulfate (SDS), 0.2% ficoll, 0.2% polyvinylpyrrolidone, 0.2% bovine serum albumin, and 50 μg/ml *E. coli* DNA, followed by washing for about 5 minutes to about 1 hour, at about 42° C. up to and including about 65° C. (inclusive of all temperatures in such range) in a 0.2×SSC buffer. Such hybridizing nucleic acid molecules preferably hybridize over substantially over their entire length. Moreover, such hybridizing nucleic acid molecules does not include previously reported nucleic acid molecules that encode effector proteins.

The delivery of effector proteins or polypeptides can be achieved in several ways: (1) as a stable transgene; (2) transiently expressed via *Agrobacterium* or viral vectors; (3) delivered by the type III secretion systems of disarmed pathogens or recombinant nonpathogenic bacteria which express a functional, heterologous type III secretion system; or (4) delivered via topical application followed by TAT protein transduction domain-mediated spontaneous uptake into cells. Each of these is discussed infra.

The DNA molecule encoding the protein or polypeptide can be incorporated in cells using conventional recombinant DNA technology. Generally, this involves inserting the DNA molecule into an expression system to which the DNA molecule is heterologous (i.e. not normally present). The heterologous DNA molecule is inserted into the expression system or vector in proper sense orientation and correct reading frame. The vector contains the necessary elements for the transcription and translation of the inserted protein-coding sequences.

U.S. Pat. No. 4,237,224 to Cohen and Boyer, which is hereby incorporated by reference in its entirety, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

Recombinant genes may also be introduced into viruses, such as vaccina virus. Recombinant viruses can be generated by transfection of plasmids into cells infected with virus.

Suitable vectors include, but are not limited to, the following viral vectors such as lambda vector system gt11, gt WES.tB, Charon 4, and plasmid vectors such as pBR322, pBR325, pACYC177, pACYC1084, pUC8, pUC9, pUC18, pUC19, pLG339, pR290, pKC37, pKC101, SV 40, pBluescript II SK +/− or KS +/− (see "Stratagene Cloning Systems" Catalog (1993) from Stratagene, La Jolla, Calif., which is hereby incorporated by reference), pQE, pIH821, pGEX, pET series (see F. W. Studier et. al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," *Gene Expression Technology* vol. 185 (1990), which is hereby incorporated by reference in its entirety), and any derivatives thereof. Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, mobilization, or electroporation. The DNA sequences are cloned into the vector using standard cloning procedures in the art, as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Laboratory, Cold Springs Harbor, N.Y. (1989), which is hereby incorporated by reference in its entirety.

A variety of host-vector systems may be utilized to express the protein-encoding sequence(s). Primarily, the vector system must be compatible with the host cell used. Host-vector systems include but are not limited to the following: bacteria transformed with bacteriophage DNA, plasmid DNA, or cosmid DNA; microorganisms such as yeast containing yeast vectors; mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); and plant cells infected by bacteria. The expression elements of these vectors vary in their strength and specificities. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements can be used.

Different genetic signals and processing events control many levels of gene expression (e.g., DNA transcription and messenger RNA (mRNA) translation).

Transcription of DNA is dependent upon the presence of a promoter which is a DNA sequence that directs the binding of RNA polymerase and thereby promotes mRNA synthesis. The DNA sequences of eukaryotic promoters differ from those of prokaryotic promoters. Furthermore, eukaryotic promoters and accompanying genetic signals may not be recognized in or may not function in a prokaryotic system, and, further, prokaryotic promoters are not recognized and do not function in eukaryotic cells.

Similarly, translation of mRNA in prokaryotes depends upon the presence of the proper prokaryotic signals which differ from those of eukaryotes. Efficient translation of mRNA in prokaryotes requires a ribosome binding site called the Shine-Dalgarno ("SD") sequence on the mRNA. This sequence is a short nucleotide sequence of mRNA that is located before the start codon, usually AUG, which encodes the amino-terminal methionine of the protein. The SD sequences are complementary to the 3'-end of the 16S rRNA (ribosomal RNA) and probably promote binding of

mRNA to ribosomes by duplexing with the rRNA to allow correct positioning of the ribosome. For a review on maximizing gene expression, see Roberts and Lauer, *Methods in Enzymology,* 68:473 (1979), which is hereby incorporated by reference in its entirety.

Promoters vary in their "strength" (i.e. their ability to promote transcription). For the purposes of expressing a cloned gene, it is desirable to use strong promoters in order to obtain a high level of transcription and, hence, expression of the gene. Depending upon the host cell system utilized, any one of a number of suitable promoters may be used. For instance, when cloning in *E. coli*, its bacteriophages, or plasmids, promoters such as the T7 phage promoter, lac promoter, trp promoter, recA promoter, ribosomal RNA promoter, the P_R and P_L promoters of coliphage lambda and others, including but not limited, to lacUV5, ompF, bla, lpp, and the like, may be used to direct high levels of transcription of adjacent DNA segments. Additionally, a hybrid trp-lacUV5 (tac) promoter or other *E. coli* promoters produced by recombinant DNA or other synthetic DNA techniques may be used to provide for transcription of the inserted gene.

Bacterial host cell strains and expression vectors may be chosen which inhibit the action of the promoter unless specifically induced. In certain operations, the addition of specific inducers is necessary for efficient transcription of the inserted DNA. For example, the lac operon is induced by the addition of lactose or IPTG (isopropylthio-beta-D-galactoside). A variety of other operons, such as trp, pro, etc., are under different controls.

Specific initiation signals are also required for efficient gene transcription and translation in prokaryotic cells. These transcription and translation initiation signals may vary in "strength" as measured by the quantity of gene specific messenger RNA and protein synthesized, respectively. The DNA expression vector, which contains a promoter, may also contain any combination of various "strong" transcription and/or translation initiation signals. For instance, efficient translation in *E. coli* requires an SD sequence about 7–9 bases 5' to the initiation codon ("ATG") to provide a ribosome binding site. Thus, any SD-ATG combination that can be utilized by host cell ribosomes may be employed. Such combinations include but are not limited to the SD-ATG combination from the cro gene or the N gene of coliphage lambda, or from the *E. coli* tryptophan E, D, C, B or A genes. Additionally, any SD-ATG combination produced by recombinant DNA or other techniques involving incorporation of synthetic nucleotides may be used.

Once the isolated DNA molecule encoding the polypeptide or protein has been cloned into an expression system, it is ready to be incorporated into a host cell. Such incorporation can be carried out by the various forms of transformation noted above, depending upon the vector/host cell system. Suitable host cells include, but are not limited to, bacteria, virus, yeast, mammalian cells, insect, plant, and the like.

Because it is desirable for recombinant host cells to secrete the encoded protein or polypeptide, it is preferable that the host cell also possess a functional type III secretion system. The type III secretion system can be heterologous to host cell (Ham et al., "A Cloned *Erwinia chrysanthemi* Hrp (Type III Protein Secretion) System Functions in *Escherichia coli* to Deliver *Pseudomonas syringae* Avr Signals to Plant Cells and Secrete Avr Proteins in Culture," *Microbiol.* 95:10206–10211 (1998), which is hereby incorporated by reference in its entirety) or the host cell can naturally possess a type III secretion system. Host cells which naturally contain a type III secretion system include many pathogenic Gram-negative bacterium, such as numerous *Erwinia* species, *Pseudomonas* species, *Xanthomonas* species, etc. Other type III secretion systems are known and still others are continually being identified. Pathogenic bacteria that can be utilized to deliver effector proteins or polypeptides are preferably disarmed according to known techniques, i.e., as described above. Alternatively, isolation of the effector protein or polypeptide from the host cell or growth medium can be carried out as described above.

Another aspect of the present invention relates to a transgenic plant which express a protein or polypeptide of the present invention and methods of making the same.

In order to express the DNA molecule in isolated plant cells or tissue or whole plants, a plant expressible promoter is needed. Any plant-expressible promoter can be utilized regardless of its origin, i.e., viral, bacterial, plant, etc. Without limitation, two suitable promoters include the nopaline synthase promoter (Fraley et al., *Proc. Natl. Acad. Sci. USA* 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus 35S promoter (O'Dell et al., "Identification of DNA Sequences Required for Activity of the Cauliflower Mosaic Virus 35S Promoter," *Nature,* 313(6005):810–812 (1985), which is hereby incorporated by reference in its entirety). Both of these promoters yield constitutive expression of coding sequences under their regulatory control.

While constitutive expression is generally suitable for expression of the DNA molecule, it should be apparent to those of skill in the art that temporally or tissue regulated expression may also be desirable, in which case any regulated promoter can be selected to achieve the desired expression. Typically, the temporally or tissue regulated promoters will be used in connection with the DNA molecule that are expressed at only certain stages of development or only in certain tissues.

In some plants, it may also be desirable to use promoters which are responsive to pathogen infiltration or stress. For example, it may be desirable to limit expression of the protein or polypeptide in response to infection by a particular pathogen of the plant. One example of a pathogen-inducible promoter is the gst1 promoter from potato, which is described in U.S. Pat. Nos. 5,750,874 and 5,723,760 to Strittmayer et al., each of which is hereby incorporated by reference in its entirety.

Expression of the DNA molecule in isolated plant cells or tissue or whole plants also requires appropriate transcription termination and polyadenylation of mRNA. Any 3' regulatory region suitable for use in plant cells or tissue can be operably linked to the first and second DNA molecules. A number of 3' regulatory regions are known to be operable in plants. Exemplary 3' regulatory regions include, without limitation, the nopaline synthase 3' regulatory region (Fraley et al., *Proc. Nat'l. Acad. Sci. USA,* 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety) and the cauliflower mosaic virus 3' regulatory region (Odell, et al., *Nature,* 313(6005):810–812 (1985), which is hereby incorporated by reference in its entirety).

The promoter and a 3' regulatory region can readily be ligated to the DNA molecule using well known molecular cloning techniques described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Press, NY (1989), which is hereby incorporated by reference in its entirety.

One approach to transforming plant cells with a DNA molecule of the present invention is particle bombardment (also known as biolistic transformation) of the host cell. This

can be accomplished in one of several ways. The first involves propelling inert or biologically active particles at cells. This technique is disclosed in U.S. Pat. Nos. 4,945,050, 5,036,006, and 5,100,792, all to Sanford, et al., each of which is hereby incorporated by reference in its entirety. Generally, this procedure involves propelling inert or biologically active particles at the cells under conditions effective to penetrate the outer surface of the cell and to be incorporated within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the heterologous DNA. Alternatively, the target cell can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (e.g., dried bacterial cells containing the vector and heterologous DNA) can also be propelled into plant cells. Other variations of particle bombardment, now known or hereafter developed, can also be used.

Another method of introducing the DNA molecule into plant cells is fusion of protoplasts with other entities, either minicells, cells, lysosomes, or other fusible lipid-surfaced bodies that contain the DNA molecule. Fraley et al., *Proc. Natl. Acad. Sci. USA,* 79:1859–63 (1982), which is hereby incorporated by reference in its entirety.

The DNA molecule may also be introduced into the plant cells by electroporation. Fromm, et al., *Proc. Natl. Acad. Sci. USA,* 82:5824 (1985), which is hereby incorporated by reference in its entirety. In this technique, plant protoplasts are electroporated in the presence of plasmids containing the DNA molecule. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and regenerate.

Another method of introducing the DNA molecule into plant cells is to infect a plant cell with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes* previously transformed with the DNA molecule. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots or roots, and develop further into plants. Generally, this procedure involves inoculating the plant tissue with a suspension of bacteria and incubating the tissue for 48 to 72 hours on regeneration medium without antibiotics at 25–28° C.

Agrobacterium is a representative genus of the Gram-negative family Rhizobiaceae. Its species are responsible for crown gall (*A. tumefaciens*) and hairy root disease (*A. rhizogenes*). The plant cells in crown gall tumors and hairy roots are induced to produce amino acid derivatives known as opines, which are catabolized only by the bacteria. The bacterial genes responsible for expression of opines are a convenient source of control elements for chimeric expression cassettes. In addition, assaying for the presence of opines can be used to identify transformed tissue.

Heterologous genetic sequences such as a DNA molecule of the present invention can be introduced into appropriate plant cells by means of the Ti plasmid of *A. tumefaciens* or the Ri plasmid of *A. rhizogenes*. The Ti or Ri plasmid is transmitted to plant cells on infection by *Agrobacterium* and is stably integrated into the plant genome. Schell, *Science,* 237:1176–83 (1987), which is hereby incorporated by reference in its entirety.

Plant tissue suitable for transformation include leaf tissue, root tissue, meristems, zygotic and somatic embryos, and anthers.

After transformation, the transformed plant cells can be selected and regenerated.

Preferably, transformed cells are first identified using, e.g., a selection marker simultaneously introduced into the host cells along with the DNA molecule of the present invention. Suitable selection markers include, without limitation, markers coding for antibiotic resistance, such as kanamycin resistance (Fraley et al., *Proc. Natl. Acad. Sci. USA,* 80:4803–4807 (1983), which is hereby incorporated by reference in its entirety). A number of antibiotic-resistance markers are known in the art and other are continually being identified. Any known antibiotic-resistance marker can be used to transform and select transformed host cells in accordance with the present invention. Cells or tissues are grown on a selection media containing an antibiotic, whereby generally only those transformants expressing the antibiotic resistance marker continue to grow.

Once a recombinant plant cell or tissue has been obtained, it is possible to regenerate a full-grown plant therefrom. Thus, another aspect of the present invention relates to a transgenic plant that includes a DNA molecule of the present invention, wherein the promoter induces transcription of the first DNA molecule in response to infection of the plant by an oomycete. Preferably, the DNA molecule is stably inserted into the genome of the transgenic plant of the present invention.

Plant regeneration from cultured protoplasts is described in Evans, et al., *Handbook of Plant Cell Cultures, Vol.* 1: (MacMillan Publishing Co., New York, 1983); and Vasil I. R. (ed.), *Cell Culture and Somatic Cell Genetics of Plants*, Acad.

Press, Orlando, Vol. I, 1984, and Vol. III (1986), each of which is hereby incorporated by reference in their entirety.

It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to, all major species of rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, cauliflower, broccoli, turnip, radish, spinach, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum, and sugarcane.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts or a petri plate containing transformed explants is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced in the callus tissue. These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is usually reproducible and repeatable.

After the DNA molecule is stably incorporated in transgenic plants, it can be transferred to other plants by sexual crossing or by preparing cultivars. With respect to sexual crossing, any of a number of standard breeding techniques can be used depending upon the species to be crossed. Cultivars can be propagated in accord with common agricultural procedures known to those in the field.

Diseases caused by the vast majority of bacterial pathogens result in limited lesions. That is, even when everything is working in the pathogen's favor (e.g., no triggering of the hypersensitive response because of R-gene detection of one of the effectors), the parasitic process still triggers defenses after a couple of days, which then stops the infection from

spreading. Thus, the very same effectors that enable parasitism to proceed must also eventually trigger defenses. Therefore, premature expression of these effectors is believed to "turn on" plant defenses earlier (i.e., prior to infection) and make the plant resistant to either the specific bacteria from which the effector protein was obtained or many pathogens. An advantage of this approach is that it involves natural products and plants seem highly sensitive to pathogen effector proteins.

According to one embodiment, a transgenic plant is provided that contains a heterologous DNA molecule of the present invention. When the heterologous DNA molecule is expressed in the transgenic plant, plant defenses are activated, imparting disease resistance to the transgenic plant. The transgenic plant can also contain an R-gene whose product is activated by the protein or polypeptide product of the heterologous DNA molecule. The R gene can be naturally occurring in the plant or heterologously inserted therein. By disease resistance, it is believed that the effector proteins of the present invention can impart to plants resistance against bacterial, viral, and/or fungal diseases.

In addition to imparting disease resistance, it is believed that stimulation of plant defenses in transgenic plants of the present invention will also result in a simultaneous enhancement in growth and resistance to insects.

Alternative to transgenic expression is topical application of the effector proteins to plants. The embodiments of the present invention where the effector polypeptide or protein is applied to the plant can be carried out in a number of ways, including: 1) application of an isolated protein (or composition containing the same) or 2) application of bacteria which do not cause disease and are transformed with a gene encoding the effector protein of the present invention. In the latter embodiment, the effector protein can be applied to plants by applying bacteria containing the DNA molecule encoding the effector protein. Such bacteria are preferably capable of secreting or exporting the protein so that the protein can contact plant cells. In these embodiments, the protein is produced by the bacteria in planta.

Such topical application can be carried out using an effector-TAT protein, which will afford transduction domain-mediated spontaneous uptake of the effector protein into cells. Basically, this is carried out by fusing an 11-amino acid peptide (YGRKKRRQRRR, SEQ ID No: 127) by standard rDNA techniques to the N-terminus of the effector protein, and the resulting tagged protein is taken up into animal cells by a poorly understood process. This peptide is the protein transduction domain (PTD) of the human immunodeficiency virus (HIV) TAT protein (Schwarze et al., "Protein transduction: unrestricted delivery into all cells?" *Trends Cell Biol.* 10:290–295 (2000), which is hereby incorporated by reference in its entirety). Other PTDs are known and can be used for this purpose (Prochiantz, "Messenger proteins: homeoproteins, TAT and others," *Curr. Opin. Cell Biol.* 12:400–406 (2000), which is hereby incorporated by reference in its entirety). See PCT Application Publication No. WO 01/19393 to Collmer et al., which is hereby incorporated by reference in its entirety.

When the effector protein is topically applied to plants, it can be applied as a composition, which includes a carrier in the form, e.g., of water, aqueous solutions, slurries, or dry powders. In this embodiment, the composition contains greater than about 5 nM of the protein of the present invention.

Although not required, this composition may contain additional additives including fertilizer, insecticide, fungicide, nematicide, and mixtures thereof. Suitable fertilizers include $(NH_4)_2NO_3$. An example of a suitable insecticide is Malathion. Useful fungicides include Captan.

Other suitable additives include buffering agents, wetting agents, coating agents, and, in some instances, abrading agents. These materials can be used to facilitate the process of the present invention.

According to one embodiment, a transgenic plant including a heterologous DNA molecule of the present invention expresses one or more effector proteins, wherein the transgenic plant is capable of supporting growth of compatible nonpathogenic bacteria. The compatible nonpathogenic bacteria can be naturally occurring or it can be recombinant. Preferably, the nonpathogenic bacteria is recombinant and expresses one or more useful products. Thus, the transgenic plant becomes a green factory for producing desirable products. Desirable products include, without limitation, products that can enhance the nutritional quality of the plant or products that are desirable in isolated form. If desired in isolated form, the product can be isolated from plant tissues. To prevent competition between the non-pathogenic bacteria which express the desired product and those that do not, it is possible to tailor the needs of recombinant, non-pathogenic bacteria so that only they are capable if living in plant tissues expressing a particular effector protein or polypeptide of the present invention.

The effector proteins or polypeptides of the present invention are believed to alter the plant physiology by shifting metabolic pathways to benefit the parasite and by activating or suppressing cell death pathways. Thus, they may also provide useful tools for efficiently altering the nutrient content of plants and delaying or triggering senescence. There are agricultural applications for all of these possible effects.

Thus, a further aspect of the present invention relates more generally to a method of modifying a metabolic pathway in a cell by introducing into the cell an effector protein or polypeptide of the present invention which interacts with a native cellular protein involved in a metabolic pathway of the cell. As a result of introducing the protein or polypeptide into the cell, the protein or polypeptide modifies the metabolic pathway through its interaction with the native cellular protein. By way of example, it is believed that HopPtoD2 is a tyrosine phosphatase that interacts with MAPK.

Yet another aspect of the present invention relates to a method of causing eukaryotic cell death which is carried out by introducing into a eukaryotic cell a protein which is cytotoxic and causes cell death. The eukaryotic cell which is treated can be either in vitro or in vivo. When treating eukaryotic cells in vivo, a number of different protein- or DNA-delivery systems can be employed to introduce the effector protein into the target eukaryotic cell.

Another aspect of the present invention relates to a method of inhibiting programmed cell death which is carried out by introducing into a eukaryotic cell susceptible to programmed cell death, a protein that is a hypersensitive response suppressor, where the introduction thereof is performed under conditions effective to inhibit programmed cell death of the eukaryotic cell. By inhibiting programmed cell death, it is intended that such inhibition includes both delaying the occurrence of programmed cell death as well as preventing programmed cell death. The eukaryotic cell which is treated can be either in vitro or in vivo. When treating eukaryotic cells in vivo, a number of different protein- or DNA-delivery systems can be employed to introduce the effector protein into the target eukaryotic cell. By way of example, hypersensitive response suppressor

proteins include, without limitation, AvrPphE$_{Pto}$, AvrPpiB1$_{Pto}$, AvrPtoB, HopPtoD1, HopPtoE, HopPtoF (previously designated AvrPphF$_{Pto}$ ORF2), and HopPtoK.

Because programmed cell death (including apoptosis) is involved in the pathogenesis of a variety of diseases, the HR suppressor proteins of the present invention can be used in the regulation thereof and, thus, as therapeutic agents in the intervention of a wide array of disease processes or maladies (see Rudin & Thompson, *Ann. Rev. Med.* 48:267–81 (1997), which is hereby incorporated by reference in its entirety).

The protein- or DNA-delivery systems can be provided in the form of pharmaceutical compositions which include the delivery system in a pharmaceutically acceptable carrier, which may include suitable excipients or stabilizers. The dosage can be in solid or liquid form, such as powders, solutions, suspensions, or emulsions. Typically, the composition will contain from about 0.01 to 99 percent, preferably from about 20 to 75 percent of active compound(s), together with the carrier, excipient, stabilizer, etc.

The compositions of the present invention are preferably administered in injectable or topically-applied dosages by solution or suspension of these materials in a physiologically acceptable diluent with a pharmaceutical carrier. Such carriers include sterile liquids, such as water and oils, with or without the addition of a surfactant and other pharmaceutically and physiologically acceptable carrier, including adjuvants, excipients or stabilizers. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose and related sugar solution, and glycols, such as propylene glycol or polyethylene glycol, are preferred liquid carriers, particularly for injectable solutions.

Alternatively, the effector proteins can also be delivered via solution or suspension packaged in a pressurized aerosol container together with suitable propellants, for example, hydrocarbon propellants like propane, butane, or isobutane with conventional adjuvants. The materials of the present invention also may be administered in a non-pressurized form such as in a nebulizer or atomizer.

Depending upon the treatment being effected, the compounds of the present invention can be administered orally, topically, transdermally, parenterally, subcutaneously, intravenously, intramuscularly, intraperitoneally, by intranasal instillation, by intracavitary or intravesical instillation, intraocularly, intraarterially, intralesionally, or by application to mucous membranes, such as, that of the nose, throat, and bronchial tubes.

Compositions within the scope of this invention include all compositions wherein the compound of the present invention is contained in an amount effective to achieve its intended purpose. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art.

One approach for delivering an effector protein into cells involves the use of liposomes. Basically, this involves providing a liposome which includes that effector protein to be delivered, and then contacting the target cell with the liposome under conditions effective for delivery of the effector protein into the cell.

Liposomes are vesicles comprised of one or more concentrically ordered lipid bilayers which encapsulate an aqueous phase. They are normally not leaky, but can become leaky if a hole or pore occurs in the membrane, if the membrane is dissolved or degrades, or if the membrane temperature is increased to the phase transition temperature. Current methods of drug delivery via liposomes require that the liposome carrier ultimately become permeable and release the encapsulated drug at the target site. This can be accomplished, for example, in a passive manner wherein the liposome bilayer degrades over time through the action of various agents in the body. Every liposome composition will have a characteristic half-life in the circulation or at other sites in the body and, thus, by controlling the half-life of the liposome composition, the rate at which the bilayer degrades can be somewhat regulated.

In contrast to passive drug release, active drug release involves using an agent to induce a permeability change in the liposome vesicle. Liposome membranes can be constructed so that they become destabilized when the environment becomes acidic near the liposome membrane (see, e.g., *Proc. Natl. Acad. Sci. USA* 84:7851 (1987); *Biochemistry* 28:908 (1989), each of which is hereby incorporated by reference in their entirety). When liposomes are endocytosed by a target cell, for example, they can be routed to acidic endosomes which will destabilize the liposome and result in drug release.

Alternatively, the liposome membrane can be chemically modified such that an enzyme is placed as a coating on the membrane which slowly destabilizes the liposome. Since control of drug release depends on the concentration of enzyme initially placed in the membrane, there is no real effective way to modulate or alter drug release to achieve "on demand" drug delivery. The same problem exists for pH-sensitive liposomes in that as soon as the liposome vesicle comes into contact with a target cell, it will be engulfed and a drop in pH will lead to drug release.

This liposome delivery system can also be made to accumulate at a target organ, tissue, or cell via active targeting (e.g., by incorporating an antibody or hormone on the surface of the liposomal vehicle). This can be achieved according to known methods.

Different types of liposomes can be prepared according to Bangham et al., *J. Mol. Biol.* 13:238–252 (1965); U.S. Pat. No. 5,653,996 to Hsu et al.; U.S. Pat. No. 5,643,599 to Lee et al.; U.S. Pat. No. 5,885,613 to Holland et al.; U.S. Pat. No. 5,631,237 to Dzau et al.; and U.S. Pat. No. 5,059,421 to Loughrey et al., each of which is hereby incorporated by reference in their entirety.

An alternative approach for delivery of effector proteins involves the conjugation of the desired effector protein to a polymer that is stabilized to avoid enzymatic degradation of the conjugated effector protein. Conjugated proteins or polypeptides of this type are described in U.S. Pat. No. 5,681,811 to Ekwuribe, which is hereby incorporated by reference in its entirety.

Yet another approach for delivery of proteins or polypeptides involves preparation of chimeric proteins according to U.S. Pat. No. 5,817,789 to Heartlein et al., which is hereby incorporated by reference in its entirety. The chimeric protein can include a ligand domain and, e.g., an effector protein of the present invention. The ligand domain is specific for receptors located on a target cell. Thus, when the chimeric protein is delivered intravenously or otherwise introduced into blood or lymph, the chimeric protein will adsorb to the targeted cell, and the targeted cell will internalize the chimeric protein, which allows the effector protein to destabilize the cell checkpoint control mechanism, affording its cytotoxic effects.

When it is desirable to achieve heterologous expression of an effector protein of the present invention in a target cell, DNA molecules encoding the desired effector protein can be delivered into the cell. Basically, this includes providing a nucleic acid molecule encoding the effector protein and then

introducing the nucleic acid molecule into the cell under conditions effective to express the effector protein in the cell. Preferably, this is achieved by inserting the nucleic acid molecule into an expression vector before it is introduced into the cell.

When transforming mammalian cells for heterologous expression of an effector protein, an adenovirus vector can be employed. Adenovirus gene delivery vehicles can be readily prepared and utilized given the disclosure provided in Berkner, *Biotechniques* 6:616–627 (1988) and Rosenfeld et al., *Science* 252:431–434 (1991), WO 93/07283, WO 93/06223, and WO 93/07282, each of which is hereby incorporated by reference in their entirety. Adeno-associated viral gene delivery vehicles can be constructed and used to deliver a gene to cells. The use of adeno-associated viral gene delivery vehicles in vitro is described in Chatterjee et al., *Science* 258:1485–1488 (1992); Walsh et al., *Proc. Nat'l. Acad. Sci.* 89:7257–7261 (1992); Walsh et al., *J. Clin Invest.* 94:1440–1448 (1994); Flotte et al., *J. Biol. Chem.* 268: 3781–3790 (1993); Ponnazhagan et al., *J. Exp. Med.* 179: 733–738 (1994); Miller et al., *Proc. Nat'l Acad. Sci.* 91:10183–10187 (1994); Einerhand et al., *Gene Ther.* 2:336–343 (1995); Luo et al., *Exp. Hematol.* 23:1261–1267 (1995); and Zhou et al., *Gene Ther.* 3:223–229 (1996), each of which is hereby incorporated by reference in their entirety. In vivo use of these vehicles is described in Flotte et al., *Proc. Nat'l Acad. Sci.* 90:10613–10617 (1993); and Kaplitt et al., *Nature Genet.* 8:148–153 (1994), each of which is hereby incorporated by reference in their entirety. Additional types of adenovirus vectors are described in U.S. Pat. No. 6,057,155 to Wickham et al.; U.S. Pat. No. 6,033, 908 to Bout et al.; U.S. Pat. No. 6,001,557 to Wilson et al.; U.S. Pat. No. 5,994,132 to Chamberlain et al.; U.S. Pat. No. 5,981,225 to Kochanek et al.; and U.S. Pat. No. 5,885,808 to Spooner et al.; and U.S. Pat. No. 5,871,727 to Curiel, each of which is hereby incorporated by reference in their entirety).

Retroviral vectors which have been modified to form infective transformation systems can also be used to deliver nucleic acid encoding a desired effector protein into a target cell. One such type of retroviral vector is disclosed in U.S. Pat. No. 5,849,586 to Kriegler et al., which is hereby incorporated by reference in its entirety.

Regardless of the type of infective transformation system employed, it should be targeted for delivery of the nucleic acid to a specific cell type. For example, for delivery of the nucleic acid into tumor cells, a high titer of the infective transformation system can be injected directly within the tumor site so as to enhance the likelihood of tumor cell infection. The infected cells will then express the desired effector protein, thereby causing cytotoxic effects.

Particularly preferred is use of the effector proteins of the present invention to treat a cancerous condition (i.e., the eukaryotic cell which is affected is a cancer cell). This can be carried out by introducing or administering to a patient, a cytotoxic *Pseudomonas* protein under conditions effective to inhibit cancer cell division, thereby treating the cancer condition.

By introducing, it is intended that the effector protein is administered to the patient, preferably in the form of a composition which will target delivery to the cancer cells. Alternatively, when using DNA-based therapies, it is intended that the introducing be carried out by administering a targeted DNA delivery system to the patient such that the cancer cells are targeted and the effector protein is expressed therein. A number of targeted delivery systems are known in the art and can be employed herewith.

EXAMPLES

The following Examples are intended to be illustrative and in no way are intended to limit the scope of the present invention.

Materials & Methods for Example 1–2

Strains and Media: *Escherichia coli* strain DH5α was used for cloning experiments, and *P. s. tomato* DC3000 or derivatives and *P. s. phaseolicola* 3121 were used for secretion or translocation assays, respectively. Routine culture conditions for bacteria are similar to those described (van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999), which is hereby incorporated by reference in its entirety). Antibiotics were used at the following concentrations: 100 μg/ml ampicillin, 20 μg/ml chloramphenicol, 10 μg/ml gentamicin, 100 μg/ml rifampicin, 10 μg/ml kanamycin, and 20 μg/ml tetracycline.

Secretion Assays: All of the secretion assays used *P. s. tomato* DC3000 strains carrying a pML123 derivative containing a PCR-cloned ORF (encoding a candidate Hrp-secreted protein) fused to nucleotide sequences that encoded either the hemagglutinin or FLAG epitopes along with their native ribosome binding sites (Labes et al., *Gene* 89:37–46 (1990), which is hereby incorporated by reference in its entirety). Details about the primers and the constructs are provided below.

HopPtoE: The hopPtoE gene was cloned using forward primer

(agtaggatccatagaaaaataccataggggtgca, SEQ ID No: 128) containing a BamHI site and reverse primer

(agtatctagatcacttgtcatcgtcgtccttgtagtcgtcaatcacatgcgcttg, SEQ ID No: 129) containing an XbaI site and FLAG epitope codons. The hopPtoC gene was cloned into plasmid vector pLN162.

HopPtoG: The hopPtoG gene was cloned using forward primer

(atgcggatcccgtatgaccttgtaaaat, SEQ ID No: 130) containing a BamHI site and reverse primer

(atgctctagatcaagcgtaatctggaa-catcgtatgggtagccgttgtaaaactgctt, SEQ ID No: 131) containing an XbaI site and HA epitope codons. The hopPtoG gene was cloned into plasmid vector pLN131.

HopPtoH: The hopPtoH gene was cloned using forward primer

(agtcggatccgataatcctggatgatccattg, SEQ ID No: 132) containing a BamHI site and reverse primer

(agtcctcgagtcacttgtcatcgtcgtccttgtagtcttgatgtgccctgtactt, SEQ ID No: 133) containing an XhoI site and FLAG epitope codons. The hopPtoH gene was cloned into plasmid vector pLN150.

HopPtoI: The hopPtoI gene was cloned using forward primer

(agtaaagcttacgggcaggtattgcaag, SEQ ID No: 134) containing a BamHI site and reverse primer

(agtatctagatcacttgtcatcgtcgtccttgtagtctttttgggcagccagcg, SEQ ID No: 135) containing an XbaI site and FLAG epitope codons. The hopPtoC gene was cloned into plasmid vector pLN165.

HopPtoL: The hopPtoL gene was cloned using forward primer

(agtaggatcctgcctccaactattggct, SEQ ID No: 136) containing a BamHI site and reverse primer

(agtatctagatcacttgtcatcgtcgtccttgtagtctctcgctttgaacgcctg, SEQ ID No: 137) containing an XbaI site and FLAG epitope codons. The hopPtoL gene was cloned into plasmid vector pLN224.

HopPtoS1: The hopPtoS1 gene was cloned using forward primer

(ataggatcccgagaacggcgcggacgtg, SEQ ID No: 138) containing a BamHI site and reverse primer

(atatctagatcatttatcatcatcatctttataatcctcgtcagagctctctgc, SEQ ID No: 139) containing an XbaI site and FLAG epitope codons. The hopPtoC gene was cloned into plasmid vector pLN142.

HopPtoS2: The hopPtoS2 gene was cloned using forward primer

(gatggatccacgcacataacaacggtg, SEQ ID No: 140) containing a BamHI site and reverse primer

(atatctagatcatttatcatcatcatctttataatcaatctgacttaatac, SEQ ID No: 141) containing an XbaI site and FLAG epitope codons. The hopPtoC gene was cloned into plasmid vector pLN223.

Constructs carrying different epitope-tagged ORFs were electroporated into DC3000 and a DC3000 hrcC mutant and grown in Hrp-inducing conditions (Yuan & He, *J. Bacteriol.* 178:6399–6402 (1996), which is hereby incorporated by reference in its entirety). Additionally, all of the DC3000 strains also carried pCPP2318, a construct that contains blaM lacking signal peptide sequences (Charkowski et al., *J. Bacteriol.* 179:3866–3874 (1997), which is hereby incorporated by reference in its entirety). DC3000 cultures were separated into cell-bound and supernatant fractions as described (van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999), which is hereby incorporated by reference in its entirety). Proteins were separated with SDS/PAGE by standard procedures (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Lab Press, Plainview, N.Y. (1989), which is hereby incorporated by reference in its entirety), transferred to polyvinylidene difluoride membranes, and immunoblotted by using anti-FLAG (Sigma), anti-hemagglutinin (Roche Molecular Biochemicals), or anti-β-lactamase (5 Prime→3 Prime) as primary antibodies. Primary antibodies were recognized by goat anti-rabbit IgG-alkaline phosphatase conjugate (Sigma), which were visualized by chemiluminescence by using a Western-Light chemiluminescence detection system (Tropix, Bedford, Mass.) and X-Omat x-ray film.

Plant Materials and Translocation Assays: *Arabidopsis thaliana* accession Columbia (Col-0) and rps2-201 (Kunkel et al., *Plant Cell* 5:865–875 (1993), which is hereby incorporated by reference in its entirety) mutant plants were grown in a growth chamber with 12 h of light at 24° C. (22° C. at night) and 70% relative humidity. Details about the primers and constructs described below.

AvrRpt2: The avrRpt2 gene was cloned using forward primer

(attggtacctctagaggatccaaccttcaatctgaa, SEQ ID No: 142) containing KpnI, XbaI, and BamHI sites and reverse primer

(atgtcgacttagcggtagagcattgcg, SEQ ID No: 143) containing an SalI site. The avrRpt2 gene was cloned into plasmid vector pÑavrRpt2.

HopPtoG-AvrRpt2: The chimeric gene was cloned using forward primer

(gcgaattcgttagttgattttgtctagcg, SEQ ID NO: 144) containing an EcoRI site, and reverse primer (gaggatccgccgttgtaaaactgcttaga, SEQ ID NO: 145) containing a BamHI site. The chimeric gene was cloned into plasmid vector phopPtoGÑavrRpt2.

The partial avrRpt2 gene with the N-terminal 40 codons deleted was amplified by using standard PCR procedures and cloned into pMOD (Epicentre Technologies, Madison, Wis.). After confirmation by sequence analysis, it was cloned into the KpnI and SalI sites of the broad-host-plasmid pLK, resulting in pΔavrRpt2. DNA fragments spanning 200 bp upstream of the Hrp boxes and the complete ORF for hopPtoG was cloned into pΔavrRpt2 to produce phopPtoG-ΔavrRpt2. The construct was introduced in *P. s. phaseolicola* 3121 by electroporation. Bacterial strains in 10 mM $MgCl_2$ at a cell density of 10^8 colony-forming units/ml were infiltrated into *A. thaliana* Col-0 and Col-0 rps2-201 plants with a needleless syringe.

Identification of Putative Effector Protein ORFs: Several approaches were employed for the identification of putative effector proteins, including the use of a Hidden Markov Model to analyze regions upstream of ORFs for hrp-related promoters (Fouts et al., *Proc. Natl. Acad. Sci. USA* 99(4): 2275–2280 (2001), which is hereby incorporated by reference in its entirety), a miniTn5gus transposon-based assay which identifies HrpL-activated insertions, via insertions downstream of Hrp boxes (Fouts et al., *Proc. Natl. Acad. Sci. USA* 99(4):2275–2280 (2001), which is hereby incorporated by reference in its entirety), and computer search for candidate Hrp-secreted proteins based on an algorithm that identifies compliance or non-compliance with export signal rules of known effector proteins (N-terminal 50 amino acids) (Petnicki-Ocwieja et al., *Proc. Natl. Acad. Sci. USA* 99:7652–7657 (2002); U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, each of which is hereby incorporated by reference in its entirety).

Materials & Methods for Example 3–8

Bacterial strains, plasmids, and media: *Escherichia coli* strains DH5α and DB3.1. (Invitrogen) were used for general cloning and Gateway technology manipulations, respectively. *P. s.* pv. *tomato* DC3000 and *P. fluorescens* strains were grown in King's B (KB) broth at 30° C. (King et al., *J. Lab. Med.* 22:301–307 (1954), which is hereby incorporated by reference in its entirety). *E. coli* and *Agrobacterium tumefaciens* C58C1 were grown in LB broth at 37° C. or 30° C., respectively. Unless otherwise noted, constructs used were made by PCR and Table 1 below includes a list of nucleotide primer sequences that were used. The pHIR11 derivative, pLN18, which lacks shcA and hopPsyA was generated as described previously (van Dijk et al., *Mol. Microbiol.* 44:1469–1481 (2002), which is hereby incorporated by reference in its entirety). Briefly, 2 kb regions upstream and downstream of shcA and hopPsyA were PCR cloned into pBluescript-II KS on either side of an nptII antibiotic marker. When transformed into the *E. coli* strain C2110 (Kahn and Hanawalt, *J. Mol. Biol.* 128:501–525 (1979), which is hereby incorporated by reference in its entirety) containing pHIR11, this construct recombined into pHIR11 because ColE1 plasmids, such as pBluescript-II KS, cannot replicate in this polA mutant at 42° C. When this strain was grown at 30° C., the ColE1 replicon replicated, forcing it to recombine out of pHIR11. pHIR11 derivatives that lacked shcA and hopPsyA were identified with PCR. Antibiotics were used at the following concentrations (μg/ml): rifampicin, 100; ampicillin, 100; gentamicin, 10; kanamycin, 50; tetracycline, 20; nalidixic acid, 20; and spectinomycin 50.

TABLE 1

Additional information on plasmid constructions

Gene Name	Primer Nucleotide Sequences (5'→3') and Other Relevant Features	SEQ ID NO:	Parent Plasmid	Plasmid Construct
shcA and	P21: gtaaaacgacggccagt	146	pHIR11	pLN18
hopPsyA	P23: atgagaattcgcatctccatgcatctt (Eco RI)	147		
	P227: cggactcgagctcagggcgcgaaactga (Xho I)	148		
	P228: gtatggtaccccgacctggcaaccgcag (Kpn I)	149		
avrPto	P792: agtcctcgagactaaagagggtatacgaatgggaaatata (Xho I)	150	pBBR1 MCS2	pLN526
	P793: agtcgatatctcattgccagttacggtacgggc (Eco RV)	151		
hopPtoT	P582: gatggatccaagtaaccggtctgcaca (Bam HI)	152	pML123	pLN256
	P583: atatctagatcatttatcatcatcatctttatatgacttttgagccgcc tg (Xba I)	153		
mouse α-Bax	P0942: ggcctcgagatggacgggtccggggagcagctt (Xho I)	154	pTA7002	pLN555
	P0943: ggcactagttcagcccatcttcttccagatggtg (Spe I)	155		
$avrPphE_{Pto}$	P683: cacctatttaattcgttgagaaacaatgaaaata	156	Gateway	pCPP5057
	P684: gacatctcgtctcgccaagcc	157	entry	
$avrPpiB1_{Pto}$	P685: caccaagcaacgtctggaggcaacaatgca	158	Gateway	pCPP5052
	P686: gtcgcctaggaaattatttagttcccatga	159	entry	
avrPtoB	P693: caccaagatcggagaggatcagaatatggcg	160	Gateway	pLN323
	P694: ggggactattctaaaagcatacttggc	161	entry	
hopPsyA	P787: caccttagcgtaaggagctaacaatgaaccc	162	Gateway	pLN458
	P788: gtttcgcgccctgagcgc	163	entry	
hopPtoE	P695: cacccataggggtgcaataacaatgaataga	164	Gateway	pLN324
	P696: gtcaatcacatgcgcttggcc	165	entry	
hopPtoF	P900: aaaaagcaggcttcgaaggagatagaaccatgtatagcccatcc	166	Gateway entry	pCPP5070
	P901: agaaagctgggtaacagacccttcgac	167		
hopPtoG	P0904: cacccacataggatatgtaaacaatgcaaataaagaac	168	Gateway	pLN520
	P0905: gccgttgtaaaactgcttagaggc	169	entry	
hopPtoK	P940: caccacaaagaggttttcaaacaatgaatc	170	Gateway	pCPP5100
	P941: gcagtagagcgtgtcgcgac	171	entry	
$avrPphE_{Pto}$	Gateway recombination		pMLl123	pCPP5068
			pPZP212	pLN535
$avrPpiB1_{Pto}$	Gateway recombination		pMLl123	pCPP5063
			pPZP212	pLN503
avrPtoB	Gateway recombination		pMLl123	pLN347
			pPZP212	pLN502
hopPsyA	Gateway recombination		pPZP212	pLN474
hopPtoE	Gateway recombination		pPZP212	pLN524
hopPtoF	Gateway recombination		pMLl123	pCPP5070
			pPZP212	pLN525
hopPtoG	Gateway recombination		pPZP212	pLN530
hopPtoK	Gateway recombination		pML123	pCPP5100
$avrPPhE_{Pto}$	P166: atacataacgctggccta	172	pKnockout-	pLN15
	P167: cggatccatgacaatcgt	173		
$avrPpiB1_{Pto}$	P168: gcaaatcctttaagctct	174	pKnockout-	pLN16
	P169: tgtttcgctaagccactg	175		
avrPtoB	P304: tcgcgccaaaccagggag	176	pKnockout-	pLN42
	P305: tcccacattctgcaacgc	177		
$hopPsyA_{Pto}$	P188: aaccccattcagtcacgc	178	pKnockout-	pLN23
	P189: tttgccatgcgtgattgc	179		
hopPtoD1	P160: cctctacgatctattcaa	180	pKnockout-	pLN4
	P161: ggcaatgctcgcggcctg	181		
hopPtoE	P913: tccggtagctcgtcagcg	182	pKnockout-	pLN543
	P914: gtggatgaccacatagttatg	183		
hopPtoF	P179: agcccatcccatacacaa	184	pKnockout-	pLN7
	P180: cactttctgtcctttggg	185		
hopPtoG	P256: tattcagcttcaagaatg	186	pKnockout-	pLN29
	P257: acccgcatagacctgtctg	187		
hopPtoH	P194: atcactccgtctcgatatc	188	pKnockout-	pLN27
	P195: tgccctgtacttcatgcg	189		
hopPtoJ	P173: ctatgtatttcaaaacac	190	pKnockout-	pLN8
	P174: atcaccctctgtaattccc	191		
hopPtoK	P171: cgcatttcaaccagctca	192	pKnockout-	pLN9
	P172: cagcaccggaagcccttc	193		
hopPtoS1	P190: ggtaatatttgtggtacttc	194	pKnockout-	pLN41
	P191: cagatgtaacgtgacatc	195		
hopPtoT	P192: acagtcagcaatcactcg	196	pKnockout-	pLN25
	P193: tacactccatacactgctg	197		
$avrPphE_{Pto}$	P854: ttgaattcatgaaaatacataacgctgg (Eco RI)	198	pGilda	pLN508
	P855: ttctcgagtcagacatctcgtctcgc (Xho I)	199		

TABLE 1-continued

Additional information on plasmid constructions

Gene Name	Primer Nucleotide Sequences (5'→3') and Other Relevant Features	SEQ ID NO:	Parent Plasmid	Plasmid Construct
$avrPpiB1_{Pto}$	P860: ttggatccgtatgcacgcaaatcctttaagctc (Bam HI)	200	pGilda	pLN507
	P861: ttctcgagtcagtcgcctaggaaattatttagttcc (Xho I)	201		
hopPtoE	P858: ttgaattcatgaatagagtttccggtagctc (Eco RI)	202	pGilda	pLN504
	P859: ttctcgagtcagtcaatcacatgcgcttgg (Xho I)	203		
hopPtoF	P856: ttgaattcatgggtaatatttgcggcacctc (Eco RI)	204	pGilda	pLN505
	P857: ttctcgagtcagacccttttcgaccgg (Xho I)	205		
hopPtoG	P862: ttgaattcatgcaaataaagaacagtcatctc (Eco RI)	206	pGilda	pLN506
	P863: ttctcgagtcagccgttgtaaaactgcttagag (Xho I)	207		

Hypersensitive Response Assays: The broad-host-range vector pML123 was used to express effector genes in Pseudomonas strains (Labes et al., *Gene* 89:37–46 (1990), which is hereby incorporated by reference in its entirety). The pML123 constructs containing hopPtoC, hopPtoD1, hopPtoD2, and hopPtoJ are described in U.S. patent application Ser. No. 10/114,828 to Collmer et al., filed Apr. 2, 2002, which is hereby incorporated by reference in its entirety; and pML123 constructs containing hopPtoE, hopPtoG, hopPtoH, hopPtoI, hopPtoL, hopPtoS1, and hopPtoS2 are described above. A pML123 construct containing hopPtoB was similarly prepared. pML123 constructs containing hopPtoF, hopPtoK, hopPtoT, avrPtoB, avrPphEPto, avrPpiB1Pto, and avrPto are detailed in Table 1. *P. fluorescens*(pHIR11) carrying pML123 constructs with effector genes or vector controls with an OD600 of 0.2 (ca. 10^8 cells/ml) in 5 mM MES (pH 5.6) and infiltrated into *Nicotiana tabacum* cv. *Xanthi, N. benthamiana*, or *A. thaliana* Ws-0 leaves. For bacterial mixing experiments involving two different *P. fluorescens* strains, *P. fluorescens*(pLN18) and a pML123 effector construct were infiltrated 2 h before *P. fluorescens*(pHIR11). The plants were scored for the production of an HR after 24 h. DC3000 strains were tested for their ability to elicit an HR on *Nicotiana tabacum* cv. *xanthi* by infiltrating strains with an OD600 of 0.2 along with 10-fold serially diluted samples with a needleless syringe.

Type III secretion assays, SDS-PAGE, and immunoblot analysis: DC3000 and DC3000 hrcC mutant (Yuan and He, *J. Bacteriol.* 178:6399–6402 (1996), which is hereby incorporated by reference in its entirety) carrying the plasmids pLN162, pLN526, pCPP2318, which encode for HopPtoE-FLAG, AvrPto, and β-lactamase, respectively, were grown in type III-inducing minimal medium (Huynh et al., *Science* 245:1374–1377 (1989), which is hereby incorporated by reference in its entirety). Cells were adjusted to an initial OD600 of 0.3 and grown for 6 h and separated into cell-bound and supernatant fractions by centrifugation at 4° C. Protein samples from bacterial cultures were prepared similarly as described (van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999), which is hereby incorporated by reference in its entirety). Cell and supernatant fractions were analyzed by SDS-PAGE (Sambrook and Russell, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), which is hereby incorporated by reference in its entirety), transferred to polyvinylidene difluoride membranes, and immunobloted using anti-AvrPto, -β-lactamase, or -FLAG as primary antibodies. Generation of anti-AvrPto antibodies has been described (van Dijk et al., *J. Bacteriol.* 181:4790–4797 (1999), which is hereby incorporated by reference in its entirety). The anti-β-lactamase antibodies were purchased from Chemicon International and the anti-FLAG antibodies were purchased from Sigma Chemical Co. Primary antibodies were recognized by goat anti-immunoglobulin G-alkaline phosphatase conjugate (Sigma Chemical Co.), and visualized by chemiluminescence using a chemiluminescence detection system and X-Omat X-ray film.

Agrobacterium-mediated transient assays: The avr gene hopPsyA was recombined into a derivative of pPZP212 (Hajdukiewicz et al., *Plant Mol. Biol.* 25:989–994 (1994), which is hereby incorporated by reference in its entirety), pLN462, which was modified to be a Gateway Destination vector, resulting in pLN474. The bax gene was PCR-cloned into pTA7002, creating pLN531, and expression of bax was induced with dexamethasome as previously described (Aoyama and Chua, *Plant Journal* 11:605–612 (1997), which is hereby incorporated by reference in its entirety). The effector genes carried on Gateway entry vectors avrPphEPto, avrPpiB1Pto, avrPtoB, hopPtoE, hopPtoF, and hopPtoG were recombined into pLN462 (which fused each gene to a hemagglutinin epitope) creating constructs pLN535, pLN503, pLN502, pLN524, pLN525, and pLN530, respectively. Agrobacterium-mediated transient expression experiments were done by infiltrating *A. tumefaciens* C58C1 (van Larebeke et al., *Nature* 252:169–170 (1974), which is hereby incorporated by reference in its entirety) harboring the disabled Ti plasmid pMP90 (Koncz and Schell, *Mol. Gen. Genet.* 204:383–396 (1986), which is hereby incorporated by reference in its entirety) at an OD600 of 0.4 into *N. benthamiana* and *N. tabacum* cv. *xanthi* plants using a needleless syringe as described (van den Ackerveken et al., *Cell* 87:1307–1316 (1996), which is hereby incorporated by reference in its entirety). For co-expression experiments, Agrobacterium strains carrying pPZP212 binary plasmids with different effector genes were infiltrated 4 h prior to infiltration of strains expressing either Bax or HopPsyA. Evidence of production of effectors from transient assays was acquired by harvesting 1 cm diameter leaf disks from infiltrated zones, grinding leaf tissue with a mortar and pestle in the presence of liquid nitrogen, and resuspending plant material in 50 μl of 1× SDS-PAGE tracking buffer. SDS-PAGE and immunoblot analysis were performed as described above using high affinity anti-hemagglutinin antibodies (Roche).

Construction of DC3000 effector mutants: In-frame internal fragments of the effector genes were PCR cloned into XcmI digested pKnockout-. (Windgassen et al., *FEMS Microbiol. Lett.* 193:201–205 (2000), which is hereby incorporated by reference in its entirety) using the primer sets listed in Table 1 above. The resulting constructs were conjugated separately into DC3000 by triparental mating using spectinomy-

cin as selection for the plasmid marker. The following effector mutants were confirmed with primers that flanked each coding region: hopPtoD1, UNL104; hopPtoC, UNL106; hopPtoE, UNL139; hopPtoK, UNL107; hopPtoJ, UNL108; hopPtoF, UNL109; avrPhEPto, UNL113; avrPpiB1Pto, UNL114; hopPtoH, UNL118; hopPtoT, UNL122; hopPtoG, UNL124; hopPtoS1, UNL126; and avrPtoB, UNL127.

Yeast viability assays: To determine whether type III effector-encoding plasmids rescued yeast from Bax-induced lethality, the effector genes avrPphEPto, avrPpiB1Pto, hopPtoG, hopPtoF, and hopPtoE were PCR-cloned into the yeast expression vector pGilda (Clontech, Palo Alto, Calif.) resulting in constructs pLN508, pLN507, pLN506, pLN505, and pLN504, respectively. Table 1 above contains information for the nucleotide primers used to make these constructs. *S. cerevisiae* EGY48 strain containing pJG4-5-Bax (kindly provided by J. C. Reed, Burnham Institute, La Jolla, Calif.) and various pGilda plasmids containing effector genes were grown in SC-U-L/glucose media overnight. The chicken Bcl-xL cloned in pGilda was kindly provided by C. Thompson (University of Chicago, Chicago, Ill.), which acted as a positive control for PCD suppression in these experiments. The yeast cultures were then serial 10-fold diluted into SC medium, and 5 μl of each dilution was dropped onto SC-U-L/Galactose or SC-UL/Glucose plates. Cells were incubated at 30° C. for 5 days, and photographed. For oxidative stress experiments, EGY48 strains containing pGilda effector constructs were grown in SC-U media overnight and treated as described in Abramovitch et al. (Abramovitch et al., *EMBO* 22:60–69 (2003), which is hereby incorporated by reference in its entirety).

Example 1

Demonstration of *Pseudomonas syringae* pv. *tomato* DC3000 Protein Secretion

From the hidden Markov model analysis, 28 candidate effector ORFs were identified that were not homologs of known Avr proteins/Hops or of any proteins unlikely to be secreted, and whose low G+C % content and association with mobile genetic elements suggested horizontal acquisition. Several of the predicted proteins shared amino acid identity with proteins likely to be effectors. For example, HopPtoS1 (ORF5) yields several ADP-ribosyltransferases in BLASTP searches (highest BLAST E value 1e-5), including a type III-secreted ADP-ribosyltransferase from *Pseudomonas aeruginosa* (Yahr et al., *Mol. Microbiol.* 22:991–1003 (1996)), and HopPtoH (ORF2) is homologous to an ORF adjacent to the avrPpiC2 avr gene of *P. s. pisi* (Arnold et al., *Microbiology* 147:1171–1182 (2001), which is hereby incorporated by reference in its entirety) (see Table 2 below).

To test whether these proteins travel the Hrp pathway, the ORFs were cloned into a broad-host-range vector fused to either the hemagglutinin or FLAG epitope. DC3000 wild-type and Hrp mutant cultures carrying these constructs were separated into supernatant and cell fractions and analyzed with SDS/PAGE and immunoblots. Five of the eight proteins tested were secreted via the DC3000 Hrp system (FIG. **1**A) and consequently were designated as HopPtoE, HopPtoG, HopPtoH, HopPtoI, and HopPtoS1, respectively. Although three ORFs (ORF6, ORF 7, and ORF8) were not detectably secreted in culture, they may still be effectors because AvrB similarly is not secreted in culture although translocated in planta (van Dijk et al., *J. Bacteriol.* 181: 4790–4797 (1999); Gopalan et al., *Plant Cell* 8:1095–1105 (1996), each of which is hereby incorporated by reference in its entirety).

TABLE 2

ORFs with 5' Hrp Promoter Sequences and Encoding Proteins Demonstrated to be Secreted by the *P. syringae* Hrp System

Initial designation	New designation	Size (bp)	% G + C	Homolog (BLASTP E value)	GenBank Accession[ŦŦ]
ORF1	HopPtoI	1,899	48.9	None	NA
ORF2[†]	HopPtoH	657	47.2	ORF3 from P. s. pisi avrPpiC2 locus (le-114)	CAC 16702
ORF3	HopPtoE	636	50.7	None	NA
ORF4	HopPtoG	1,482	43.7	Hypothetical protein from *R. solanacearum* (le-137)	NP_521884
ORF5[‡]	HopPtoS1	852	46.5	Chicken ADP-ribosyltransferase (1e-5)	P55807

[ŦŦ]Each of the listed Genbank Accessions is hereby incorporated by reference in its entirety.
[†]ORF2: homolog described in Arnold et al., Microbiology 147:1171-1182 (2001), which is hereby incorporated by reference in its entirety.
[‡]ORF5: homolog described in Tsuchiya et al., J.Biol.Chem. 269:27451-27457 (1994), which is hereby incorporated by reference in its entirety. Determined to possess an ART domain (pfam1129), further confirming its similarity to ADP-ribosyltransferases.

To determine whether the export signal-based search had identified any novel Hrp-secreted proteins, secretion assays were also performed on ORF29 and ORF30, both of which seemed to be particularly promising candidates. The products encoded by ORF29 and ORF30 share similarity with a putative type III effector from *S. enterica*, SrfC, and ADP-ribosyltransferases, respectively. Both ORFs were PCR-cloned into a broad-host-range vector fused to the FLAG epitope, and each construct was introduced into DC3000 wild-type and Hrp mutant strains. The epitope-tagged ORF29 and ORF30 proteins were secreted by DC3000 in a Hrp-dependent manner without leakage of a cytoplasmic marker protein (FIG. **1**B), and consequently they were designated as HopPtoL and HopPtoS2, respectively (see Table 3 below).

TABLE 3

Selected ORFs Encoding Candidate Effector Proteins That Were Identified by the Genomewide Search Based on Export-Signal Patterns

Designation	New Designation	Size (bp)	% G + C'	Hrp promoter[ŧ]	Mobile DNA[†]	Homolog (BLASTP E value)	GenBank Accession[‡]
ORF29[§]	HopPtoL	2700	61.0	n	n	SPI-2 regulated SrfC (1e-21)	AAF74575
ORF30[Ω,¶]	HopPtoS2	795	46.5	y	n	Clostridium exoenzyme C3 ADP ribosyl-Tansferase (1e-5)	NP_346979
ORF31[ε,¶]	NA	897	49.8	y	y	Chicken ADP ribosyl-transferase (5e-3)	P55807
ORF32[ε,¶]	NA	507	54.2	y	y	Chicken ADP ribosyl-transferase (5e-3)	P55807
ORF33[Θ]	NA	2823	55.2	n	y	SepC insecticidal toxin (1e-128)	NP_065279
ORF34*	NA	534	63.5	y	n	Lytic enzyme (3e-36)	BAA83137

[ŧ]Indicates that the ORF is within 10 kb of a HrpL-responsive Hrp promoter identified in Fouts
[†]Indicates that a transposon, plasmid, or a phage-related sequence is within 10 kb.
[‡]Each of the listed Genbank Accessions is hereby incorporated by reference in its entirety.
[¶]ORF was determined to possess an ART domain (pfam1129), further confirming its similarity to ADP-ribosyltransferases.
[§]Homolog identified in Worley et al., Mol. Microbiol. 36:749-761 (2000), which is hereby incorporated by reference in its entirety.
[Ω]Homolog identified in Nolling et al., J. Bacteriol. 183:4823-4838 (2001), which is hereby incorporated by reference in its entirety.
[ε]Homolog identified in Tsuchiya et al., J. Biol. Chem. 269:27451-27457 (1994), which is hereby incorporated by reference in its entirety.
[Θ]Homolog identified in Hurst et al., J. Bacteriol. 182:5127-5138 (2000), which is hereby incorporated by reference in its entirety.
*Homolog identified in Nakayama et al., Mol. Microbiol. 38:213-231 (2000), which is hereby incorporated by reference in its entirety.

Interestingly, the export signal-based search found a putative effector, SrfC, that is predicted to travel the type III pathway encoded by SPI2 of *S. enterica* (Worley et al., *Mol. Microbiol.* 36:749–761 (2000), which is hereby incorporated by reference in its entirety). A further indicator of the efficacy of the search was the finding of three additional ADP-ribosyltransferases, ORF 30, 31, and 32, all with significant amino acid sequence identity to HopPtoS 1 (Table 3).

Example 2

AvrRpt2 Translocation Assay Indicates that at Least One of the Additional Hops Is Translocated into Plant Cells.

HopPtoG was selected to test for translocation into plant cells because it shared no similarities with any sequences in the databases and was shown to be secreted (FIG. **1**B). *P. s. phaseolicola* carrying a plasmid expressing hopPtoG-Δ avrRpt2 elicited an RPS2-dependent hypersensitive response in *A. thaliana* Col-0 (FIG. **1**C), indicating that targeting information in HopPtoG directed translocation of the AvrRpt2 fusion protein into plant cells. Thus, HopPtoG appears to be a Hrp-injected effector protein.

Discussion of Examples 1–2

One demonstration of the selectivity of the export signal rules is that only the chicken ADP-ribosyltransferase $NRT2_{CHK}$ shows major violations of the rules even though this protein is more similar to HopPtoS1 and S2 than either of the type III-secreted ADP-ribosyltransferases from *P. aeruginosa*, ExoS and ExoT (see Petnicki-Ocwieja et al., *Proc. Natl. Acad. Sci. USA* 99:7652–7657 (2002); U.S. patent application Ser. No. 10/341,180 to Collmer et al., filed Jan. 13, 2003, each of which is hereby incorporated by reference in its entirety).

HopPtoS1 and HopPtoS2 share sequence similarity with ADP-ribosyltransferases, proteins that have long been implicated in bacterial pathogenesis in animals through the modification of host signal transduction pathways (Finlay & Falkow, *Microbiol. Mol. Biol. Rev.* 61:136–169 (1997), which is hereby incorporated by reference in its entirety), but until now have not been implicated in the bacterial pathogenesis of plants. The DC3000 genomic studies described in Fouts et al. (*Proc. Natl. Acad. Sci. USA* 99:2275–2280 (2002), which is hereby incorporated by reference in its entirety) clearly show that several of the effectors in DC3000 are redundant. By using the pattern-based export prediction, three ADP-ribosyltransferase genes (in addition to hopPtoS1) that have N-termini putative export signals were identified in the genome of DC3000. One of these, ORF32, appears to be truncated. The other two, HopPtoS2 and ORF31, are full-length genes based on sequence alignments. HopPtoS2 is secreted by the Hrp system (FIG. **1**B) and ORF31 shares high amino acid sequence identity with the Hrp-secreted HopPtoS1. Interestingly, HopPtoS1 contains putative myristoylation and palmitoylation sites at its N terminus, whereas the other two do not, indicating that HopPtoS1 may be localized to the plasma membrane. Thus, there appear to be at least three Hrp-secreted ADP-ribosyltransferases and these may localize to different regions of the plant cell. The existence of

these proteins in *Pseudomonas syringae* is particularly noteworthy given that ADP-ribosyltransferase genes have not been identified in the bacterial plant pathogen genomes that have been published thus far (Simpson et al., *Nature* 406: 151–159 (2000); Wood et al., *Science* 294:2317–2323 (2001); Goodner et al., *Science* 294:2323–2328 (2001); Salanoubat et al., *Nature* 415:497–502 (2002), each of which is hereby incorporated by reference in its entirety). Significantly, the genomewide search for export signals yielded a homolog of the *S. enterica* candidate effector SrfC, further adding to the growing list of effectors shared between plant and animal pathogens. It is also noteworthy that one of the ORFs found by the genomewide search (ORF48) is a homolog of a bacterial catalase (BLASTP 1e-126), and another (ORF49) is a glucokinase homolog (BLASTP 3e-42). These putative effectors likely have a role in oxidative stress and regulation of sugar metabolism, respectively.

Example 3

HopPtoE Suppresses the Hypersensitive Response in Tobacco and a DC3000 hopPtoE Mutant Possesses an Enhanced Hypersensitive Response Phenotype

In the course of experiments with confirmed DC3000 type III effectors, the effector HopPtoD2 was observed capable of suppressing the HR elicited by *P. s. phaseolicola* on *Nicotiana benthamiana* plants. These results prompted the screening other effector proteins for HR suppressor activity (Collmer et al., *Trends Microbiol.* 10:462–470 (2002)). To do this, the pHIR11 system was used, allowing nonpathogens such as *E. coli* and *P. fluorescens* to elicit the HR and secrete effectors in culture via the TTSS. This tool allowed for testing whether individual effectors were capable of suppressing the HopPsyA-dependent HR as depicted in FIG. **2**A. *P. fluorescens*(pHIR11) strains carrying a number of different effector constructs were infiltrated into tobacco (*N. tabacum* cv. *xanthi*). Interestingly, HopPtoD2, the effector that suppressed an HR elicited by *P. phaseolicola*, did not suppress the HopPsyA-dependent HR (FIG. **4**A). The first identified effector to suppress or block the HR elicited by *P. fluorescens*(pHIR11) was HopPtoE (FIG. **2**B). To detect a potential phenotype consistent with HopPtoE acting as an HR suppressor, a DC3000 mutant defective in HopPtoE was constructed. Both DC3000 and the hopPtoE mutant, UNL139, elicited an HR in tobacco when infiltrated into leaf panels at high inoculum (FIG. **2**C).

Based on this result, it is likely that effectors have functionally redundant roles, which may partially mask a phenotype. Therefore, a more sensitive HR assay was performed, where 10-fold serially diluted bacterial strains were infiltrated into tobacco leaf panels to detect any subtle difference in the 5 ability of different strains of bacteria to elicit an HR. When UNL139 was tested in this assay, it was more effective than DC3000 at HR elicitation at lower cell density (FIG. **2**C). Interestingly, when hopPtoE was provided in trans to UNL139, the mutant strain was less effective at HR elicitation than DC3000 (FIG. **2**C). Thus, the enhanced HR phenotype of the hopPtoE mutant was complemented by hopPtoE. These observations are consistent with HopPtoE acting as an HR suppressor and suggest that HopPtoE contributes incrementally to the ability of the pathogen to suppress the HR.

Example 4

HopPtoE Does Not Block the DC3000 Type III Secretion System

One possible explanation for the observed phenotypes was that HopPtoE was blocking the type III secretion of other type III substrates, including Avr proteins. There is actually a precedent for type III substrates, such as HrpZ and HrpW, to block the type III secretion of proteins from *P. syringae* (Alfano et al., *Mol. Microbiol.* 19:715–728 (1996); Charkowski et al., *J. Bacteriol.* 180:5211–5217 (1998), each of which is hereby incorporated by reference in its entirety) and it was crucial to consider this alternative. To test this, DC3000 and a DC3000 hrcC mutant defective in the TTSS, both carrying plasmids that contained avrPto and hopPtoE, were grown in a medium that induced type III secretion. These cultures were separated into supernatant and cell fractions, and analyzed them by SDS-PAGE and immunoblots with either anti-FLAG or -AvrPto antibodies. Both AvrPto and HopPtoE were secreted in culture via the TTSS (FIG. **3**B), indicating that, at least in culture, over-expression of hopPtoE did not block type III secretion. It was next determined whether expression of hopPtoE in DC3000 altered its HR-eliciting ability. Because DC3000 contains a native copy of hopPtoE in its genome, these experiments actually tested whether over-expression of HopPtoE altered the HR phenotype. DC3000 strains, with and without plasmid-encoded hopPtoE, were infiltrated into tobacco at high inoculum levels (10^8 cells/ml). After 24 hours, DC3000 elicited an HR on tobacco, whereas DC3000 with a plasmid containing hopPtoE did not (FIG. **3**B), indicating that over-expression of HopPtoE suppressed the HR. However, after approximately 3 h, DC3000 with hopPtoE in trans also elicited an HR. Thus, hopPtoE in trans in DC3000 only delayed the ability of this pathogen to elicit an HR. When these experiments were repeated in *N. benthamiana*, the HR delay was greater than 24 h, indicating that the suppression ability of HopPtoE depended to a certain extent on the test plant. To eliminate the possibility that HopPtoE affected the ability of *P. fluorescens*(pHIR11) to deliver the Avr protein HopPsyA into plant cells, a different bacterial strain was used to deliver HopPsyA (as compared to the strain used to deliver HopPtoE) into plant cells. To accomplish this, a pHIR11 derivative, pLN18, was constructed so as to lack hopPsyA and shcA, a gene that encodes a chaperone for HopPsyA (van Dijk et al., *Mol. Microbiol.* 44:1469–148 (2002), which is hereby incorporated by reference in its entirety). *P. fluorescens*(pLN18) does not elicit an HR on tobacco because it lacks HopPsyA (FIG. **3**C), while maintaining the ability to secrete proteins via its functional TTSS.

In planta mixed-inoculum experiments were performed by first infiltrating into tobacco *P. fluorescens*(pLN18) with hopPtoE contained in a broad-host-range plasmid and, after 2 h, *P. fluorescens*(pHIR11). *P. fluorescens*(pHIR11) was infiltrated at an OD600 sufficient to cause HR elicitation. FIG. **3**C shows that *P. fluorescens*(pLN18) retained the ability to suppress the pHIR11-dependent HR. This indicates that the HR suppression activity does not occur in the bacterial cell.

Example 5

pHIR11 Assays Identify Seven Effectors Capable of Suppressing the HopPsyA-Dependent Hypersensitive Response

Nineteen confirmed effector genes were cloned into a broad-host-range plasmid and tested to determine whether the encoded effectors were able to suppress the HR elicited by *P. fluorescens*(pHIR11) (see FIG. **4**A for a list of the effectors tested). Each candidate suppressor gene was expressed in *P. fluorescens*(pHIR11) and these strains were infiltrated into tobacco and *Arabidopsis thaliana* ecotype Ws-0, two plants that produce an HR in response to pHIR11-containing bacteria.

Surprisingly, seven of the nineteen effectors tested were able to suppress the pHIR11-dependent HR on both *A.*

thaliana and tobacco (FIGS. **4**B–C). In planta mixed-inoculum experiments similar to those describe in FIG. **3**C demonstrated that all of the identified suppressors were able to inhibit the pHIR11-dependent HR. These results indicate that the site of suppressor activity was outside of the bacteria. Two of the identified suppressors, HopPtoF and AvrPtoB, were homologs of AvrPphF and VirPphA, respectively, two Avr proteins able to "block" the HR produced by *P. s. phaseolicola* (Jackson et al., *Proc. Natl. Acad. Sci. USA* 96:10875–10880 (1999); Tsiamis et al., *EMBO J.* 19:3204–3214 (2000), each of which is hereby incorporated by reference in its entirety). The VirPphA homolog, AvrPtoB, was recently reported to suppress the HR elicited by AvrPto (Abramovitch et al., *EMBO J.* 22:60–69 (2003), which is hereby incorporated by reference in its entirety). Thus, these findings demonstrate that AvrPtoB and HopPtoF are HR suppressors. The other HR suppressors identified were $AvrPphE_{Pto}$, $AvrPpiB1_{Pto}$, HopPtoD1, and HopPtoK. The HR suppression observed for HopPtoD1 and HopPtoK was not complete (i.e., the HR was present, although much reduced).

Example 6

Agrobacterium Transient Assays that Co-Deliver HopPsyA and Individual Hypersensitive Response Suppressors Confirm that Each Effector Alone Suppresses the HopPsyA-Dependent Hypersensitive Response Inside Plant Cells

To determine if the HR suppression is due solely to the suppressor proteins, both HopPsyA and individual HR suppressor effectors were transiently co-delivered using *Agrobacterium*-mediated transient assays (agroinfitrations) (van den Ackerveken et al., *Cell* 87:1307–1316 (1996), which is hereby incorporated by reference in its entirety). In each case, the effector suppressed the HopPsyA-dependent HR (FIG. **5**A). Protein expression was confirmed with immunoblots that showed the agroinfiltrations produced both HopPsyA and the specific suppressor tested (FIG. **5**B). These data complement the bacteria-delivered suppressor data shown above, because agroinfiltrations demonstrate that the suppressor activity is dependent only on the suppressor and that the suppressor acts within plant cells, whereas the experiments where *P. fluorescens*(pHIR11) deliver each suppressor resemble what happens in nature and protein levels are closer to the levels that the pathogen "inject" into plant cells.

Example 7

DC3000 Suppressor Mutants Display an Enhanced Ability to Elicit a Hypersensitive Response on Nonhost Plants, Consistent with Loss of Hypersensitive Response Suppression Activity in the Pathogen

Based on the above findings, it was recognized that a pathogen may encode multiple HR suppressors, each contributing, perhaps incrementally, to the suppression of the HR and/or plant defenses. To analyze these proteins in more detail, mutants defective in each gene corresponding to the effectors listed in FIG. **4**A were made. The ability of DC3000 and the suppressor mutants to induce defense responses on non-host plants were tested, similar to the experiments described in FIG. **2**C. Tobacco leaves were infiltrated with different dilutions of DC3000 or each mutant, and then their ability to elicit an HR was analyzed. Interestingly, all the mutants were more effective at eliciting an HR at lower concentrations, generally producing an HR at 10-fold higher dilution than wild type DC3000 (FIG. **6**). As an example, UNL105 caused a confluent HR at a titer of 10^6 cells/ml, whereas DC3000 only produced a spotty HR or no HR at this titer. It is important to note that DC3000 produced a typical HR at dilutions of 10^6 cells/ml or higher. This enhanced HR phenotype produced by each suppressor mutant resulted from the absence of the effector, because when each was supplied in trans the HR-eliciting ability returned to a DC3000-like HR (FIG. **6**).

Although HopPtoG was not identified as an HR suppressor in the assays with *P. fluorescens*(pHIR11), the hopPtoG mutant UNL124 caused an enhanced HR phenotype. Moreover, additional assays shown below suggest that HopPtoG does function as a suppressor. Thus, these findings demonstrate that the phenotype of potential suppressor mutants on non-host plants is consistent with and complements HR suppression data. Therefore, the HR titration assays should be useful in the identification of other HR suppressors in bacterial plant pathogens.

Example 8

Pseudomonas syringae Hypersensitive Response Suppressors Inhibit Programmed Cell Death Induced by the Pro-apoptotic Protein Bax in both Plants and Yeast

The pro-apoptotic mouse protein Bax has been shown to induce PCD in plants that resembles the HR (Kawai-Yamada et al., *Proc. Natl. Acad. Sci. USA* 98:12295–12300 (2001); Lacomme and Santa Cruz, *Proc. Natl. Acad. Sci. USA* 96:7956–7961 (1999), each of which is hereby incorporated by reference in its entirety). Bax is a member of the Bcl-2 family of pro-apoptotic proteins and is thought to initiate programmed cell death ("PCD") by localizing to the mitochondria and causing the release of pro-apoptotic factors, including cytochrome c (Jurgensmeier et al., *Proc. Natl. Acad. Sci. USA* 95:4997–5002 (1998), which is hereby incorporated by reference in its entirety). Recently, Abramovitch et al. (*EMBO* J. 22:60–69 (2003), which is hereby incorporated by reference in its entirety) reported that AvrPtoB suppresses Bax-induced PCD in plants. The suppressors identified in Examples 3–7 were tested in their ability to suppress Bax-induced PCD in plants. With the exception of $AvrPpiB1_{Pto}$, all of them suppressed Bax-induced cell death in plants (FIG. **7**A). Interestingly, AvrPphE, HopPtoG, HopPtoF, and HopPtoE also suppressed Bax-induced PCD in yeast (FIG. **7**B). The fact that AvrPtoB was unable to suppress Bax-induced PCD in yeast highlights a difference between the activity of these suppressors. Moreover, AvrPphE, HopPtoG, HopPtoF, and HopPtoE were unable to suppress the PCD initiated in yeast by H_2O_2, while AvrPtoB did suppress PCD in this assay (Abramovitch et al., *EMBO J.* 22:60–69 (2003), which is hereby incorporated by reference in its entirety). This further demonstrates that the PCD suppressors display different PCD suppressing characteristics.

Discussion of Examples 3–8

Effectors delivered by the Hrp TTSS appear central to *P. syringae* pathogenesis, but the anti-host functions of these proteins remain obscure. The above Examples identify a founding inventory of Hrp effectors from *P. s. tomato* DC3000 using several novel bioassays and provide evidence that many of these proteins appear to suppress one or more broadly conserved eukaryote PCD pathways. To understand these results, it is useful to consider the collection of

effectors that were assayed, the utility and limitations of the bioassays, and the role of plant cell death in disease and defense. The nineteen effectors considered here were recently identified in DC3000 on the basis of their homology with known effectors and/or their ability to be secreted and/or translocated by the Hrp TTSS. In general, *P. syringae* TTSS effectors identified on the basis of avirulence phenotypes are designated Avrs, whereas those identified through secretion assays are designated Hops. However, the working assumption is that all of the "Avrs" are injected into plant cells by the Hrp system and many of the "Hops" will confer avirulence phenotypes to bacteria if tested in hosts that happen to carry a corresponding R gene; that is, effectors, Avrs, and Hops are synonymous terms.

It must be noted that the effector described herein do not represent the entire inventory of DC3000 effectors. Effectors encoded within the Hrp pathogenicity island are described elswhere (Alfano et al., *Proc. Natl. Acad. Sci. USA* 97:4856–4861 (2000), which is hereby incorporated by reference in its entirety. Additional candidate effectors in DC3000 have also been identified (Collmer et al., *Trends Microbiol.* 10:462–470 (2002), which is hereby incorporated by reference in its entirety).

However, the set of effectors analyzed here suggests that many DC3000 effectors have HR suppression activity. The bioassays used herein were designed to efficiently detect HR suppressor activity, determine whether suppressor action occurs in plant cells rather than in bacteria, and determine if the test effectors could also suppress PCD in other plants and the model eukaryote, yeast. The primary screen, based on suppression of the HR elicited by *P. fluorescens*(pHIR11) in tobacco, proved to be simple and effective (FIG. **2**). Although there is the formal possibility that suppressors identified with this bioassay could be merely interfering with the delivery of HopPsyA, multiple lines of evidence indicate that they act after delivery into plant cells. For example, HopPtoE overexpression had no effect on the secretion of AvrPto (FIG. **3**A), a representative type III substrate, and HopPtoE suppressed HopPsyA-dependent HR elicitation when delivered by a functional TTSS in a different strain (FIG. **3**C) or when transiently expressed in plant cells following inoculation with *A. tumefaciens* (FIG. **5**A). It is also noteworthy that the suppressors identified herein functioned when delivered via the TTSS, a natural route that is thought to yield relatively low levels of effectors within plant cells. Agrobacterium-mediated transient expression, in contrast, can produce far higher levels of effectors within plant cells potentially leading to artifactual responses. It should also be noted that HopPtoD1 and HopPtoK appear to exhibit limited suppressor activity.

In an attempt to identify plant targets or sites of action of the suppressors in plants, HopPtoE, AvrPphE$_{Pto}$, AvrPiB1$_{Pto}$, AvrPtoB, HopPtoF, and HopPtoG were subjected to cursory bioinformatic analyses. BLASTP and PSI-BLAST searches (Altschul et al., *Nucleic Acids Res.* 25: 3389–3402 (1997), which is hereby incorporated by reference in its entirety) did not identify any proteins (other than clear Avr homologs) that shared significant similarity with any of the suppressors. However, 3D-PSSM analyses, a method that uses protein fold recognition to identify proteins with similar folding patterns (Kelley et al., *J. Mol. Biol.* 299:499–520 (2000), which is hereby incorporated by reference in its entirety), indicated that AvrPtoB had similarity to heme-dependent peroxidases (above 90% certainty; PSSM E value 0.0895). Moreover, when AvrPtoB was aligned with a lignin peroxidase, a representative heme-dependent peroxidase (Welinder, *Eur. J. Biochem.* 151: 497–504 (1985), which is hereby incorporated by reference in its entirety), the amino acids within the peroxidase active site were present similarly spaced in AvrPtoB. This result is intriguing because of the clear involvement of reactive oxygen species (ROS) in plant defense (Mittler, *Trends Plant Sci.* 7:405–410 (2002), which is hereby incorporated by reference in its entirety) and the potential of peroxidases to modulate ROS. Moreover, there have been reports of peroxidases rescuing Bax-induced cell death in yeasts (Kampranis et al., *J. Biol. Chem.* 275:29207–29216 (2000); Moon et al., *Biochem. Biophys. Res. Commun.* 290:457–462 (2002), each of which is hereby incorporated by reference in its entirety) and transgenic antisense tobacco plants with reduced amounts of ascorbate peroxidase were "hyperresponsive" to *P. syringae* (Mittler et al., *Proc. Natl. Acad. Sci. USA* 96:14165–14170 (1999), which is hereby incorporated by reference in its entirety), producing a phenotype reminiscent of the enhanced HR phenotypes produced by the suppressor mutants reported here. However, Abramovitch et al. (*EMBO* J. 22:60–69 (2003), which is hereby incorporated by reference in its entirety) reported that AvrPtoB possessed predicted structural features similar to domains within Bcl-2 family members, an equally intriguing finding due to the involvement of these proteins in PCD regulation. Yeast has emerged as model for studying PCD and has proven particularly useful for the analysis of cell death inducers and suppressors obtained from multicellular eukaryotes with more complex PCD pathways (Madeo et al., *Curr. Genet.* 41:208–216 (2002), which is hereby incorporated by reference in its entirety). An example of the utility of the yeast system to plant PCD research is found in the induction of yeast PCD by the plant defense protein osmotin (Narasimhan et al., *Mol. Cell* 8:921–930 (2001), which is hereby incorporated by reference in its entirety). A particularly fruitful use of the yeast system involves heterologous expression of the mammalian Bax protein, which induces PCD in yeast. Yeast expressing Bax can be screened, as done here, for heterologously expressed genes that block Bax-induced PCD. This system has been used to identify the *Arabidopsis* ethylene-responsive element binding protein (AtEBP) as a suppressor of PCD (Pan et al., *FEBS Lett.* 508:375–378 (2001), which is hereby incorporated by reference in its entirety) and its relevance to plant biology is further indicated by observations that Bax expression in tobacco can induce an apparent HR and that Bcl-2 (an anti-aptototic gene of the Bax/Bcl-2 family) expression in tobacco strongly alters plant-pathogen interactions (Dickman et al., *Proc. Natl. Acad. Sci. USA* 98:6957–6962 (2001); Lacomme and Santa Cruz, *Proc. Natl. Acad. Sci. USA* 96:7956–7961 (1999), each of which is hereby incorporated by reference in its entirety).

Four of the five effectors tested (AvrPphE$_{Pto}$, HopPtoG, HopPtoF, and HopPtoE) suppress Bax-induced yeast PCD, indicating that the targets are likely to be broadly conserved and not unique to plants. Interestingly, AvrPpiB1$_{Pto}$ and AvrPtoB failed to do so, even though both suppressed the HR elicited by *P. fluorescens*(pHIR11) in both tobacco and *Arabidopsis*, and DC3000 avrPtoB and avrPpiB1Pto mutants produced enhanced HRs. It is also puzzling that HopPtoG failed to suppress the HR elicited by *P. fluorescens* (pHIR11) although a DC3000 hopPtoG mutant had enhanced HR activity and HopPtoG suppressed Bax-induced yeast PCD. Moreover, it is also noteworthy that HopPtoD2, an effector that was recently identified to suppresses an HR elicited by avirulent *P. syrinage* strains did not suppress the HR elicited by *P. fluorescens*(pHIR11).

These exceptions suggest that multiple bioassays will be required to identify all of the DC3000 effectors with some ability to suppress PCD.

While the suppressors described here were identified due to their ability to suppress PCD, it is possible they suppress other more general plant defenses as well. Indeed, HopPtoD2 has been found to be an active protein tyrosine phosphatase that appears to modulate a mitogen-activated protein kinase (MAPK) pathway in tobacco. An analogous MAPK pathway in *Arabidopsis* is part of the plant innate immune system activated in response to bacterial flagellin (Asal et al., *Nature* 415:977–983 (2002); Felix et al., *Plant J.* 18:265–276 (1999), each of which is hereby incorporated by reference in its entirety). The innate immune systems of mammals, insects, and plants have the capacity to recognize common markings on microorganisms, such as flagellin or LPS (Boller, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 46:189–214 (1995); Medzhitov and Janeway, *Trends Microbiol.* 8:452–456 (2000), each of which is hereby incorporated by reference in its entirety). These common components have been referred to as pathogen-associated molecular patterns (PAMPs) and they are not known to elicit the HR in plants. Thus, the assays used herein would not detect the activity of suppressors that specifically targeted PAMP-induced defense pathways unless the target was at convergence points of PCD pathways and PAMP-induced innate immunity pathways. Future research will determine whether these PCD suppressors specifically target Avr-induced PCD pathways or also suppress other plant defenses generally grouped into a broad category of defenses typically referred to as non-host resistance (Heath, *Curr. Opin. Plant Biol.* 3:315–319 (2000), which is hereby incorporated by reference in its entirety).

A general model of suppressor function must also reconcile several behaviors of bacterium-plant interactions that involve multiple effectors. Expression in *P. syringae* of a heterologous effector typically results in HR elicitation in test plants that carry a corresponding R gene despite the presence of resident suppressor effectors. For example, DC3000 heterologously expressing avrRpt2 or avrRps4 elicits the HR in *Arabidopsis* plants carrying the corresponding R genes (Hinsch and Staskawicz, *Mol. Plant—Microbe Interact.* 9:55–61 (1996); Kunkel et al., *Plant Cell* 5:865–875 (1993), which is hereby incorporated by reference in its entirety). On the other hand, suppressors can block HR elicitation by resident effectors, as revealed by the original discovery of suppressors like VirPphA and effectors with masked avirulence activity in *P. s. phaseolicola* (Jackson et al., *Proc. Natl. Acad. Sci. USA* 96:10875–10880 (1999), which is hereby incorporated by reference in its entirety) and by the observations presented here that several effectors can block HR elicitation by HopPsyA in the heterologous *P. fluorescens*(pHIR11) system. Perhaps the simplest explanation is that there is a hierarchy in the delivery of effectors by wild-type strains. Such a hierarchy in delivery has been proposed to explain the deployment of effectors with conflicting activities, such as the *Salmonella* SopE and SptP proteins, in animal pathogens (Cornelis and van Gujsegem, *Annu. Rev. Microbiol.* 54:734–774 (2000); Galán and Zhou, *Proc. Natl. Acad. Sci. USA* 97:8754–8761 (2000), each of which is hereby incorporated by reference in its entirety). The global identification of a set of suppressors in *P. s. tomato* DC3000 should facilitate systematic investigation of the underlying functions of TTSS effectors in *P. syringae* pathogenesis.

A final aspect of PCD and pathogenesis is that the ability to elicit host cell death appears to be a general characteristic of TTSS-dependent pathogens like *P. syringae* despite the fact that these bacteria typically rely upon living host cells as sites of multiplication (Alfano and Collmer, *J. Bacteriol.* 179:5655–5662 (1997); Knodler and Finlay, *Microbes Infect.* 3:1321–1326 (2001), each of which is hereby incorporated by reference in its entirety). This is particularly puzzling with *P. syringae* because late-stage infections with most strains produce necrotic lesions, but the symptomless growth of *P. s. syringae* gacS mutants suggests that such cell killing maybe gratuitous (Willis et al., *Mol. Plant—Microbe Interact.* 3:149–156 (1990), which is hereby incorporated by reference in its entirety). Similarly puzzling are recent observations suggesting that plants compromised in PCD pathways are unexpectedly more resistant to *P. syringae* (Lincoln et al., *Proc. Natl. Acad. Sci. USA* 99:15217–15221 (2002); Stone et al., *Plant Cell* 12:1811–1822 (2000); Richael et al., *Physiol. Mol. Plant Pathol.* 59:213–221 (2001), each of which is hereby incorporated by reference in its entirety). Thus, rapid and delayed host cell death are associated with defense and disease, respectively, and pathogen manipulation of cell death pathways may be a central process in pathogenesis.

Although the invention has been described in detail for the purposes of illustration, it is understood that such detail is solely for that purpose, and variations can be made therein by those skilled in the art without departing from the spirit and scope of the invention which is defined by the following claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 209

<210> SEQ ID NO 1
<211> LENGTH: 1899
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 1

atgcttatcg ggcacagctt gcatcacatg cgacccactg ctgtggattc tagcctacca 60

acttccgcaa ctagccagac tatcagcaat accaaaagtc ggctggatcc gcatcgtgtc 120

cgtgaactta cattcatcgg agtgggtagt agtgttgcct acctactcaa tgagcttaat 180

-continued

```
ggtcgctttg ccgatagcgg ggtaacaacg ccgtttttag gaaaagtcag tattgtaggc    240

aaggacgact cttgggccga gaatgttcgt gggaaaggtt atattaacca ccagactgaa    300

attataagcc aatgggacca acaggttcca aaatatgatc ctaactatgc tgctcgtgcc    360

gaattttctg cgagtaaccg aagacagttg acgcgaacag tggagttagg cgcagaacat    420

ttgaaagcac aggtaacagg catttcgcga ttggatgacg gttgttttcg aataaatctg    480

gacaatggcc agattttgca aagccgacag attgtactgg ggactggtgc cggaccccat    540

accagtatct ggaacagcgt tacatcacac actcaagcag aaaaacgact ggacaacatc    600

aaattgcatg agcagaaagc cttgcgtggc aaggtgctgg acctggatga gtttatgcga    660

gcgagtgatg cctctcccca gacgtttgct ggaaaaacgg tggtgataca tggaccaaat    720

gcaggcattg atgcagctga acgtgccggg gagcttgggg caaatgcggt ttggtttacc    780

cgcagtacga atccggtatt gctggatggc aatcaactaa aattcgcgcc agagctggcc    840

aaaagcgcta tacataaagt tgacaaatta gatattcgcc caacaaaact agagaatggt    900

ttcgcattgc gactacatta cagttcgcta ggacaagact cacgggagcc aaagaaggtg    960

ctagatgcgg actattatgt gtacgccatg ggtcaagata ttcataagcc gggtagcgca   1020

gcggccatac taggcagtct tcttgaccac ctagaaccta tatatgacta cgatcaagtc   1080

tatagcgacc agcctttcaa gacagtaata ggcttgcaaa gtcgcggctc caatagcgat   1140

aatggtttaa ttattgtcgg ggcggcagtt gctcagctgg ccactaatgt tcagcatagc   1200

tataaggacc acgcgttgga tcgtatactt gaggaaatga ccaggctccc cgaaaagcaa   1260

acagaaaagc tatcacaaat gctgttagaa ggtgcgccat cagtacagat ccagacatat   1320

ctaaaaacct ggcagttaga tagcggtcaa ccgccagata aacaggtact gcagaatcaa   1380

gtagaaaact atctggcggc ccgagactac ttccagcggc aaaccaacga acaaaagggc   1440

aacctggacg gggttgccgc agaggtaaaa aatcaaacct taaccgaggt tgcatcggtc   1500

atcgtgtcac cacagttagg cacgatcaag gcctccgctg cagcattgtc gggacttatg   1560

ccagcatatg tggctaacgg cgaaaataac tttaccaccg ataatcgaac tatgctccgt   1620

gccggcattg cagcaagata tccgaatata ggtaacgctg aagccagtgc atttatcgat   1680

gaagtagtaa ctttgcgtca ccttaatagt cagcgtttta ttgagaaggt agcaggcgaa   1740

atgatggaca aaggagctca accactggtg tcgttacgcc ccccggtcct aggtgtcccg   1800

gcgtcggtca ggactgctta tgaggcttac ttgcacgcgc tgaattctgg agcgcacgat   1860

ggtacgccgt taagtcagcg ctggctgccc aaaaaatag                          1899
```

<210> SEQ ID NO 2
<211> LENGTH: 632
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 2

```
Met Leu Ile Gly His Ser Leu His His Met Arg Pro Thr Ala Val Asp
  1               5                  10                  15

Ser Ser Leu Pro Thr Ser Ala Thr Ser Gln Thr Ile Ser Asn Thr Lys
             20                  25                  30

Ser Arg Leu Asp Pro His Arg Val Arg Glu Leu Thr Phe Ile Gly Val
         35                  40                  45

Gly Ser Ser Val Ala Tyr Leu Leu Asn Glu Leu Asn Gly Arg Phe Ala
     50                  55                  60
```

-continued

```
Asp Ser Gly Val Thr Thr Pro Phe Leu Gly Lys Val Ser Ile Val Gly
 65                  70                  75                  80

Lys Asp Asp Ser Trp Ala Glu Asn Val Arg Gly Lys Gly Tyr Ile Asn
                 85                  90                  95

His Gln Thr Glu Ile Ile Ser Gln Trp Asp Gln Gln Val Pro Lys Tyr
            100                 105                 110

Asp Pro Asn Tyr Ala Ala Arg Ala Glu Phe Ser Ala Ser Asn Arg Arg
        115                 120                 125

Gln Leu Thr Arg Thr Val Glu Leu Gly Ala Glu His Leu Lys Ala Gln
    130                 135                 140

Val Thr Gly Ile Ser Arg Leu Asp Asp Gly Cys Phe Arg Ile Asn Leu
145                 150                 155                 160

Asp Asn Gly Gln Ile Leu Gln Ser Arg Gln Ile Val Leu Gly Thr Gly
                165                 170                 175

Ala Gly Pro His Thr Ser Ile Trp Asn Ser Val Thr Ser His Thr Gln
            180                 185                 190

Ala Glu Lys Arg Leu Asp Asn Ile Lys Leu His Glu Gln Lys Ala Leu
        195                 200                 205

Arg Gly Lys Val Leu Asp Leu Asp Glu Phe Met Arg Ala Ser Asp Ala
    210                 215                 220

Ser Pro Gln Thr Phe Ala Gly Lys Thr Val Val Ile His Gly Pro Asn
225                 230                 235                 240

Ala Gly Ile Asp Ala Ala Glu Arg Ala Gly Glu Leu Gly Ala Asn Ala
                245                 250                 255

Val Trp Phe Thr Arg Ser Thr Asn Pro Val Leu Leu Asp Gly Asn Gln
            260                 265                 270

Leu Lys Phe Ala Pro Glu Leu Ala Lys Ser Ala Ile His Lys Val Asp
        275                 280                 285

Lys Leu Asp Ile Arg Pro Thr Lys Leu Glu Asn Gly Phe Ala Leu Arg
    290                 295                 300

Leu His Tyr Ser Ser Leu Gly Gln Asp Ser Arg Glu Pro Lys Lys Val
305                 310                 315                 320

Leu Asp Ala Asp Tyr Tyr Val Tyr Ala Met Gly Gln Asp Ile His Lys
                325                 330                 335

Pro Gly Ser Ala Ala Ala Ile Leu Gly Ser Leu Leu Asp His Leu Glu
            340                 345                 350

Pro Ile Tyr Asp Tyr Asp Gln Val Tyr Ser Asp Gln Pro Phe Lys Thr
        355                 360                 365

Val Ile Gly Leu Gln Ser Arg Gly Ser Asn Ser Asp Asn Gly Leu Ile
    370                 375                 380

Ile Val Gly Ala Ala Val Ala Gln Leu Ala Thr Asn Val Gln His Ser
385                 390                 395                 400

Tyr Lys Asp His Ala Leu Asp Arg Ile Leu Glu Glu Met Thr Arg Leu
                405                 410                 415

Pro Glu Lys Gln Thr Glu Lys Leu Ser Gln Met Leu Leu Glu Gly Ala
            420                 425                 430

Pro Ser Val Gln Ile Gln Thr Tyr Leu Lys Thr Trp Gln Leu Asp Ser
        435                 440                 445

Gly Gln Pro Pro Asp Lys Gln Val Leu Gln Asn Gln Val Glu Asn Tyr
    450                 455                 460

Leu Ala Ala Arg Asp Tyr Phe Gln Arg Gln Thr Asn Glu Gln Lys Gly
465                 470                 475                 480
```

-continued

```
Asn Leu Asp Gly Val Ala Ala Glu Val Lys Asn Gln Thr Leu Thr Glu
                485                 490                 495

Val Ala Ser Val Ile Val Ser Pro Gln Leu Gly Thr Ile Lys Ala Ser
            500                 505                 510

Ala Ala Ala Leu Ser Gly Leu Met Pro Ala Tyr Val Ala Asn Gly Glu
        515                 520                 525

Asn Asn Phe Thr Thr Asp Asn Arg Thr Met Leu Arg Ala Gly Ile Ala
    530                 535                 540

Ala Arg Tyr Pro Asn Ile Gly Asn Ala Glu Ala Ser Ala Phe Ile Asp
545                 550                 555                 560

Glu Val Val Thr Leu Arg His Leu Asn Ser Gln Arg Phe Ile Glu Lys
                565                 570                 575

Val Ala Gly Glu Met Met Asp Lys Gly Ala Gln Pro Leu Val Ser Leu
            580                 585                 590

Arg Pro Pro Val Leu Gly Val Pro Ala Ser Val Arg Thr Ala Tyr Glu
        595                 600                 605

Ala Tyr Leu His Ala Leu Asn Ser Gly Ala His Asp Gly Thr Pro Leu
    610                 615                 620

Ser Gln Arg Trp Leu Pro Lys Lys
625                 630
```

<210> SEQ ID NO 3
<211> LENGTH: 657
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 3

```
atgatcactc cgtctcgata tccaggcatc tatatcgccc ccctcagtaa cgaaccgaca     60

gcagctcaca catttaaaga acaagcagag gaagcacttg accatatcag cgccgcaccc    120

tctggcgata agctattgcg aaaaatatcc actcttgcca gtcaaaaaga tagaaaagtc    180

acgctaaaag agattgaaat aaataaccag tgttataccg aagctgttct gagcagragg    240

caactggaaa agtacgaacc agaaaacttt aacgagaacc ggcacattgc atcacagcta    300

tcacgaaagg ggacctttac caaaggtgaa ggaagcaacg cgattattgg ctggtcacca    360

gacaaagcaa gcatacgctt aaatcagaat ggctcaccgt tacaccttgg aatggataac    420

gacgacaaaa tcacgaccct agctcatgag ctcgttcatg ctcgacatgt gttaggtggc    480

agctccttag cggatggcgg agatcgctat aatccacgta cgggatctgg caaagaggaa    540

cttagggccg ttggattaga taagtaccgc tattcactta caaaaaaacc gtcagagaac    600

tccatccgag ctgaacacgg cctgcctctg cgcatgaagt acagggcaca tcaatag       657
```

<210> SEQ ID NO 4
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 4

```
Met Ile Thr Pro Ser Arg Tyr Pro Gly Ile Tyr Ile Ala Pro Leu Ser
  1               5                  10                  15

Asn Glu Pro Thr Ala Ala His Thr Phe Lys Glu Gln Ala Glu Glu Ala
             20                  25                  30

Leu Asp His Ile Ser Ala Ala Pro Ser Gly Asp Lys Leu Leu Arg Lys
         35                  40                  45

Ile Ser Thr Leu Ala Ser Gln Lys Asp Arg Lys Val Thr Leu Lys Glu
     50                  55                  60
```

-continued

```
Ile Glu Ile Asn Asn Gln Cys Tyr Thr Glu Ala Val Leu Ser Arg Arg
 65                  70                  75                  80

Gln Leu Glu Lys Tyr Glu Pro Glu Asn Phe Asn Glu Asn Arg His Ile
                 85                  90                  95

Ala Ser Gln Leu Ser Arg Lys Gly Thr Phe Thr Lys Gly Glu Gly Ser
            100                 105                 110

Asn Ala Ile Ile Gly Trp Ser Pro Asp Lys Ala Ser Ile Arg Leu Asn
        115                 120                 125

Gln Asn Gly Ser Pro Leu His Leu Gly Met Asp Asn Asp Asp Lys Ile
    130                 135                 140

Thr Thr Leu Ala His Glu Leu Val His Ala Arg His Val Leu Gly Gly
145                 150                 155                 160

Ser Ser Leu Ala Asp Gly Gly Asp Arg Tyr Asn Pro Arg Thr Gly Ser
                165                 170                 175

Gly Lys Glu Glu Leu Arg Ala Val Gly Leu Asp Lys Tyr Arg Tyr Ser
            180                 185                 190

Leu Thr Lys Lys Pro Ser Glu Asn Ser Ile Arg Ala Glu His Gly Leu
        195                 200                 205

Pro Leu Arg Met Lys Tyr Arg Ala His Gln
    210                 215


<210> SEQ ID NO 5
<211> LENGTH: 636
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 5

atgaatagag tttccggtag ctcgtcagcg acttggcagg cagtcaacga tcttgtggag     60

caagtaagcg agagaaccac gttgtctacg acaggttatc agacggcaat gggccgcttg    120

aacaaaccgg aaaaatcaga tgcggatgcg ctgatgacta tgaggagggc gcaacagtac    180

acggatagcg cgaagcgaac ttatatttcg gaaacgctga tgaatctggc agatttgcag    240

caaaggaaaa tctatcgcac caacagcggg aacttgcgtg gcgcgattga gatgacgcct    300

acgcaactca cagattgcgt acagaagtgc cgcgaagagg ggttctccaa ttgtgacata    360

caggcgctgg aaatcggctt gcaccttcga cataagttag gaatctcaga tttcaccatc    420

tacagcaacc gtaagttaag ccataactat gtggtcatcc accccagcaa tgcatttccg    480

aaaggagcga ttgtagactc ttggacggga cagggcgtgg tggagctgga cttcaagacc    540

cgattgaaat tcaagcaccg ggaagagaac tacgcagtga acgccaatat gcacgagtgg    600

atcgagagat acggccaagc gcatgtgatt gactga                              636


<210> SEQ ID NO 6
<211> LENGTH: 211
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 6

Met Asn Arg Val Ser Gly Ser Ser Ser Ala Thr Trp Gln Ala Val Asn
  1               5                  10                  15

Asp Leu Val Glu Gln Val Ser Glu Arg Thr Thr Leu Ser Thr Thr Gly
             20                  25                  30

Tyr Gln Thr Ala Met Gly Arg Leu Asn Lys Pro Glu Lys Ser Asp Ala
         35                  40                  45

Asp Ala Leu Met Thr Met Arg Arg Ala Gln Gln Tyr Thr Asp Ser Ala
     50                  55                  60
```

-continued

```
Lys Arg Thr Tyr Ile Ser Glu Thr Leu Met Asn Leu Ala Asp Leu Gln
 65                  70                  75                  80

Gln Arg Lys Ile Tyr Arg Thr Asn Ser Gly Asn Leu Arg Gly Ala Ile
                 85                  90                  95

Glu Met Thr Pro Thr Gln Leu Thr Asp Cys Val Gln Lys Cys Arg Glu
            100                 105                 110

Glu Gly Phe Ser Asn Cys Asp Ile Gln Ala Leu Glu Ile Gly Leu His
        115                 120                 125

Leu Arg His Lys Leu Gly Ile Ser Asp Phe Thr Ile Tyr Ser Asn Arg
    130                 135                 140

Lys Leu Ser His Asn Tyr Val Val Ile His Pro Ser Asn Ala Phe Pro
145                 150                 155                 160

Lys Gly Ala Ile Val Asp Ser Trp Thr Gly Gln Gly Val Val Glu Leu
                165                 170                 175

Asp Phe Lys Thr Arg Leu Lys Phe Lys His Arg Glu Glu Asn Tyr Ala
            180                 185                 190

Val Asn Ala Asn Met His Glu Trp Ile Glu Arg Tyr Gly Gln Ala His
        195                 200                 205

Val Ile Asp
    210
```

<210> SEQ ID NO 7
<211> LENGTH: 1482
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 7

```
atgcaaataa agaacagtca tctctattca gcttcaagaa tggtgcagaa tacttttaat     60

gcctcgccta agatggaagt aactaatgca atagcaaaaa ataatgaacc tgctgcgctg    120

agcgctacgc aaactgcaaa gacacacgaa ggcgattcaa aaggccaatc cagcaataac    180

tctaaattgc ccttccgcgc catgaggtac gctgcatacc ttgcaggcag cgcctacctc    240

tacgataaaa ctgccaataa ttttttttctt tctaccactt ctctgcatga tggcaaaggt    300

ggttttacca gcgatgccag gcttaacgat gcacaagata aagcgcgaaa gcgctaccaa    360

aacaaccata gcagcactct tgaaaataaa aactcgcttt taagcccgct taggctttgc    420

ggagagaatc agttcttaac gatgattgat tatcgtgcag caactaagat ttacctctcc    480

gacctagttg acacggagca agcgcacaca tcaattctga agaatattat gtgcctgaaa    540

ggtgagctta ccaatgaaga ggcaataaaa aaactcaacc cggaaaaaac accaaaagac    600

tatgacctta caaatagcga agcctatata agcaagaaca aatattcttt gaccggcgtt    660

aaaaatgagg agacgggatc tactggttat acatctcgtt ctatcacaaa gccatttgtg    720

gaaaaaggcc tgaaacactt tataaaagcg actcatggcg aaaaagctct cacgcccaag    780

cagtgtatgg aaactcttga taacttactt cgaaaaagta tcacgctcaa cagtgattcc    840

caattcgcag caggccaggc acttttggtt ttcagacagg tctatgcggg tgaagacgct    900

tgggggggatg cggaacgggt catattgaaa agccattata atcggggcac tgtactccaa    960

gatgaagctg ataaaataga actaagtagg ccgttctcag agcaagattt agcaaagaac   1020

atgtttaaga ggaataccag cattgcaggg ccagtgctct accacgcata tatttatata   1080

caagaaaaaa tcttcaagct acccccccgac aaaatagaag atttgaaaca taaatcaatg   1140

gcagacttga aaaacctgcc tttgactcat gttaagctta gcaattccgg tgtgggattt   1200

gaagacgcct cagggttagg agactcgttt acagctctca acgcgacgtc ctgtgttaat   1260
```

-continued

```
cacgcaagaa taatgagtgg tgagcctccc ttgtcaaaag atgatgttgt gattctgata   1320

ggttgcctca acgccgtata cgacaattcg agcggaataa ggcattctct ccgcgaaatt   1380

gcacgagggt gctttgtggg tgctggtttt acggtccagg acggtgacga cttctacaaa   1440

cagatctgca aaaacgcctc taagcagttt tacaacggct aa                      1482


<210> SEQ ID NO 8
<211> LENGTH: 493
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 8

Met Gln Ile Lys Asn Ser His Leu Tyr Ser Ala Ser Arg Met Val Gln
  1               5                  10                  15

Asn Thr Phe Asn Ala Ser Pro Lys Met Glu Val Thr Asn Ala Ile Ala
             20                  25                  30

Lys Asn Asn Glu Pro Ala Ala Leu Ser Ala Thr Gln Thr Ala Lys Thr
         35                  40                  45

His Glu Gly Asp Ser Lys Gly Gln Ser Ser Asn Asn Ser Lys Leu Pro
     50                  55                  60

Phe Arg Ala Met Arg Tyr Ala Ala Tyr Leu Ala Gly Ser Ala Tyr Leu
 65                  70                  75                  80

Tyr Asp Lys Thr Ala Asn Asn Phe Phe Leu Ser Thr Thr Ser Leu His
                 85                  90                  95

Asp Gly Lys Gly Gly Phe Thr Ser Asp Ala Arg Leu Asn Asp Ala Gln
            100                 105                 110

Asp Lys Ala Arg Lys Arg Tyr Gln Asn Asn His Ser Ser Thr Leu Glu
        115                 120                 125

Asn Lys Asn Ser Leu Leu Ser Pro Leu Arg Leu Cys Gly Glu Asn Gln
    130                 135                 140

Phe Leu Thr Met Ile Asp Tyr Arg Ala Ala Thr Lys Ile Tyr Leu Ser
145                 150                 155                 160

Asp Leu Val Asp Thr Glu Gln Ala His Thr Ser Ile Leu Lys Asn Ile
                165                 170                 175

Met Cys Leu Lys Gly Glu Leu Thr Asn Glu Glu Ala Ile Lys Lys Leu
            180                 185                 190

Asn Pro Glu Lys Thr Pro Lys Asp Tyr Asp Leu Thr Asn Ser Glu Ala
        195                 200                 205

Tyr Ile Ser Lys Asn Lys Tyr Ser Leu Thr Gly Val Lys Asn Glu Glu
    210                 215                 220

Thr Gly Ser Thr Gly Tyr Thr Ser Arg Ser Ile Thr Lys Pro Phe Val
225                 230                 235                 240

Glu Lys Gly Leu Lys His Phe Ile Lys Ala Thr His Gly Glu Lys Ala
                245                 250                 255

Leu Thr Pro Lys Gln Cys Met Glu Thr Leu Asp Asn Leu Leu Arg Lys
            260                 265                 270

Ser Ile Thr Leu Asn Ser Asp Ser Gln Phe Ala Ala Gly Gln Ala Leu
        275                 280                 285

Leu Val Phe Arg Gln Val Tyr Ala Gly Glu Asp Ala Trp Gly Asp Ala
    290                 295                 300

Glu Arg Val Ile Leu Lys Ser His Tyr Asn Arg Gly Thr Val Leu Gln
305                 310                 315                 320

Asp Glu Ala Asp Lys Ile Glu Leu Ser Arg Pro Phe Ser Glu Gln Asp
                325                 330                 335
```

-continued

```
Leu Ala Lys Asn Met Phe Lys Arg Asn Thr Ser Ile Ala Gly Pro Val
            340                 345                 350

Leu Tyr His Ala Tyr Ile Tyr Ile Gln Glu Lys Ile Phe Lys Leu Pro
        355                 360                 365

Pro Asp Lys Ile Glu Asp Leu Lys His Lys Ser Met Ala Asp Leu Lys
    370                 375                 380

Asn Leu Pro Leu Thr His Val Lys Leu Ser Asn Ser Gly Val Gly Phe
385                 390                 395                 400

Glu Asp Ala Ser Gly Leu Gly Asp Ser Phe Thr Ala Leu Asn Ala Thr
                405                 410                 415

Ser Cys Val Asn His Ala Arg Ile Met Ser Gly Glu Pro Pro Leu Ser
            420                 425                 430

Lys Asp Asp Val Val Ile Leu Ile Gly Cys Leu Asn Ala Val Tyr Asp
        435                 440                 445

Asn Ser Ser Gly Ile Arg His Ser Leu Arg Glu Ile Ala Arg Gly Cys
    450                 455                 460

Phe Val Gly Ala Gly Phe Thr Val Gln Asp Gly Asp Asp Phe Tyr Lys
465                 470                 475                 480

Gln Ile Cys Lys Asn Ala Ser Lys Gln Phe Tyr Asn Gly
                485                 490
```

<210> SEQ ID NO 9
<211> LENGTH: 852
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 9

```
atgggtaata tttgtggtac ttctggctcc aatcatgtgt atagtccgcc tattagccct     60

caacatgcat ctggttcgtc cacaccagtg cccagtgctt ctgggacgat gctttctctc    120

agtcatgaac aaatattaag ccagaactat gctagcaata taaaggggaa atatcgcacg    180

aacccccgaa aaggaccatc tcctaggctt tctgatacgc tgatgaagca ggcgctgtct    240

tcagtgatca cacaagagaa aaagcgactt aaaagtcaac caaagtcaat agcccaagat    300

attcagcctc caaacagcat gatcaaaaat gcacttgatg aaaaagacag ccacccttttt    360

ggtgattgct tttcagacga tgaatttctt gcgatccatc tctatacgag ttgtctttac    420

agaccgatca accatcatct gcggtatgcc ccgaaaaatg atgtcgcgcc tgttgtcgag    480

gcaatgaata gcggtttggc caaacttgct caataccctg attatcaggt gtctggtcag    540

ctgcatagag gcatcaagca aaagatggat gatggtgaag ttatgagtcg cttcaagccg    600

ggtaatactt atcgtgatga cgcgttcatg agcacatcga ctagaatgga tgttacagaa    660

gaatttactt ccgatgtcac gttacatctg cagtcctcat cagccgtcaa tataggtccc    720

ttttcaaaaa acccatacga ggacgaagcg ctcatcccgc ccctgacgcc tttcaaagta    780

accggtctgc acaagcagga cgataggtgg cacgtccact tgaacgagat cgcagagagc    840

tctgacgagt ga                                                        852
```

<210> SEQ ID NO 10
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 10

```
Met Gly Asn Ile Cys Gly Thr Ser Gly Ser Asn His Val Tyr Ser Pro
  1               5                  10                  15

Pro Ile Ser Pro Gln His Ala Ser Gly Ser Ser Thr Pro Val Pro Ser
             20                  25                  30

Ala Ser Gly Thr Met Leu Ser Leu Ser His Glu Gln Ile Leu Ser Gln
         35                  40                  45

Asn Tyr Ala Ser Asn Ile Lys Gly Lys Tyr Arg Thr Asn Pro Arg Lys
     50                  55                  60

Gly Pro Ser Pro Arg Leu Ser Asp Thr Leu Met Lys Gln Ala Leu Ser
 65                  70                  75                  80

Ser Val Ile Thr Gln Glu Lys Lys Arg Leu Lys Ser Gln Pro Lys Ser
                 85                  90                  95

Ile Ala Gln Asp Ile Gln Pro Pro Asn Ser Met Ile Lys Asn Ala Leu
            100                 105                 110

Asp Glu Lys Asp Ser His Pro Phe Gly Asp Cys Phe Ser Asp Asp Glu
        115                 120                 125

Phe Leu Ala Ile His Leu Tyr Thr Ser Cys Leu Tyr Arg Pro Ile Asn
    130                 135                 140

His His Leu Arg Tyr Ala Pro Lys Asn Asp Val Ala Pro Val Val Glu
145                 150                 155                 160

Ala Met Asn Ser Gly Leu Ala Lys Leu Ala Gln Tyr Pro Asp Tyr Gln
                165                 170                 175

Val Ser Gly Gln Leu His Arg Gly Ile Lys Gln Lys Met Asp Asp Gly
            180                 185                 190

Glu Val Met Ser Arg Phe Lys Pro Gly Asn Thr Tyr Arg Asp Asp Ala
        195                 200                 205

Phe Met Ser Thr Ser Thr Arg Met Asp Val Thr Glu Glu Phe Thr Ser
    210                 215                 220

Asp Val Thr Leu His Leu Gln Ser Ser Ser Ala Val Asn Ile Gly Pro
225                 230                 235                 240

Phe Ser Lys Asn Pro Tyr Glu Asp Glu Ala Leu Ile Pro Pro Leu Thr
                245                 250                 255

Pro Phe Lys Val Thr Gly Leu His Lys Gln Asp Asp Arg Trp His Val
            260                 265                 270

His Leu Asn Glu Ile Ala Glu Ser Ser Asp Glu
        275                 280
```

<210> SEQ ID NO 11
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 11

```
atgagcttat cgccgacgct gcaaaagcta actaatatat tgggcccgac aaaaaatgcc     60

aagcctgtca cagaggctat ccagtggcag gaaggcatgg atataacgct gcatgtcagc    120

ggcgacagcc ttaccttact agctaaaatc atagaactgc gtacagaccc taaagacgac    180

attttattgc gcaagctgct tacccatacg tttccgggcc tgcgtctgcg ccgtggcgcg    240

cttaccatca accctgatga aagtgccctg gttttctctt atgaacacga ttttcacctt    300

ctggacaaag cccgttttga gagcctgctg gccaactttg ctgaaacggc gcaggagctt    360

cgagacacag cgacacattt tcgttttaac tga                                 393
```

-continued

<210> SEQ ID NO 12
<211> LENGTH: 130
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 12

Met Ser Leu Ser Pro Thr Leu Gln Lys Leu Thr Asn Ile Leu Gly Pro
1 5 10 15

Thr Lys Asn Ala Lys Pro Val Thr Glu Ala Ile Gln Trp Gln Glu Gly
20 25 30

Met Asp Ile Thr Leu His Val Ser Gly Asp Ser Leu Thr Leu Leu Ala
35 40 45

Lys Ile Ile Glu Leu Arg Thr Asp Pro Lys Asp Asp Ile Leu Leu Arg
50 55 60

Lys Leu Leu Thr His Thr Phe Pro Gly Leu Arg Leu Arg Arg Gly Ala
65 70 75 80

Leu Thr Ile Asn Pro Asp Glu Ser Ala Leu Val Phe Ser Tyr Glu His
85 90 95

Asp Phe His Leu Leu Asp Lys Ala Arg Phe Glu Ser Leu Leu Ala Asn
100 105 110

Phe Ala Glu Thr Ala Gln Glu Leu Arg Asp Thr Ala Thr His Phe Arg
115 120 125

Phe Asn
130

<210> SEQ ID NO 13
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 13

atgaaacaac gagcgacagt catctgcaaa cgtgacggcc aggtgcttta cgtacgcaaa 60

ccaaaatccc gctgggcttt gccaggtggc aagattgaag ccggggaaac gcctttccag 120

gctgccgtgc gcgagctttg cgaagaaacc ggtctggaaa atctcgatct gttgtacctg 180

gcggtgtacg agaaaggtga ggtcacgcac tacgtgttca ccactcaggt tcctgcctac 240

agcgagcctt cgccccagaa cgagatttct gcctgcaaat ggcttgcgcc caaaaatctt 300

ggcgacctta aggccagcag cgcgaccaag gctatcgtca agtcgtatgg ccgccaggct 360

gaagacggtt tactcagcgc taactag 387

<210> SEQ ID NO 14
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 14

Met Lys Gln Arg Ala Thr Val Ile Cys Lys Arg Asp Gly Gln Val Leu
1 5 10 15

Tyr Val Arg Lys Pro Lys Ser Arg Trp Ala Leu Pro Gly Gly Lys Ile
20 25 30

Glu Ala Gly Glu Thr Pro Phe Gln Ala Ala Val Arg Glu Leu Cys Glu
35 40 45

Glu Thr Gly Leu Glu Asn Leu Asp Leu Leu Tyr Leu Ala Val Tyr Glu
50 55 60

Lys Gly Glu Val Thr His Tyr Val Phe Thr Thr Gln Val Pro Ala Tyr
65 70 75 80

-continued

```
Ser Glu Pro Ser Pro Gln Asn Glu Ile Ser Ala Cys Lys Trp Leu Ala
                85                  90                  95

Pro Lys Asn Leu Gly Asp Leu Lys Ala Ser Ser Ala Thr Lys Ala Ile
            100                 105                 110

Val Lys Ser Tyr Gly Arg Gln Ala Glu Asp Gly Leu Leu Ser Ala Asn
        115                 120                 125
```

<210> SEQ ID NO 15
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 15

```
gtgctcgctt ttgcatacgt cagcctgatt agagagcaga aattggacat caaaaaacgt     60

tggccttcca gtgagcagga gttggtagaa gtccgacggt ttaacaaaac cctcgcccgg    120

ctgccgcgtt tccaggttcg caatcgcctc acgccccgct tgattcaggc gctgctgcgg    180

gcggctcaga ttggtcgcgc gttgaaaccg gtcaaacatg acctgcggat tgaaacaacc    240

atcgtcagca ccggtaacgt ccctgtttca gtgcgaatca taaggcccaa aggcaaaccc    300

aaaggcgtgg tgtttgatat tcacggcggc ggttgggtga tcggcaacgc ccagatgaac    360

gatgacctca atatcggtat cgttaacgcg tgcaacgtgg cggtcgtgtc cgttgattac    420

agattggctt tatcgacccc cgtcgaaggg ctgatggatg actgcttttc tgccgcatgc    480

tggctgctgg gtagcgactg taaggagttt gccggcctgc cggttattgt cgtcggtgag    540

tccgcgggcg ggcatcttgc cgcagccact ttgctcaaat tgaaagccag gcccgacttg    600

ctcaagcgcg tagtcggcac ggttctgtat tacggcgtgt acgacctgac cgggacaaaa    660

agcgttcgta ccgcaggccc ggaaacgctg gtgctcgacg gcccgggcat ggtcggcgca    720

atgcgcttgc tcgccccgga cagaaccgac gagaagcgcc gcgagccgcc gttatcgccc    780

ttgtatggcg acctcacgga tctgccgccc gccctgatgt ttgtcggcga actcgacccg    840

ctgctggacg acacgctgga aatggccgag cgatggaaaa actcggcaga cgttgaaatg    900

catcttctgc ccgagtctcc acatgggttc atccacttcc cgactgcctt ggcgcgcaag    960

gtacttgcgc gcagccacga gtggataaac gcgaggatgg aaggacggcc ttaa         1014
```

<210> SEQ ID NO 16
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 16

```
Val Leu Ala Phe Ala Tyr Val Ser Leu Ile Arg Glu Gln Lys Leu Asp
  1               5                  10                  15

Ile Lys Lys Arg Trp Pro Ser Ser Glu Gln Glu Leu Val Glu Val Arg
             20                  25                  30

Arg Phe Asn Lys Thr Leu Ala Arg Leu Pro Arg Phe Gln Val Arg Asn
         35                  40                  45

Arg Leu Thr Pro Arg Leu Ile Gln Ala Leu Leu Arg Ala Ala Gln Ile
     50                  55                  60

Gly Arg Ala Leu Lys Pro Val Lys His Asp Leu Arg Ile Glu Thr Thr
 65                  70                  75                  80

Ile Val Ser Thr Gly Asn Val Pro Val Ser Val Arg Ile Ile Arg Pro
                85                  90                  95

Lys Gly Lys Pro Lys Gly Val Val Phe Asp Ile His Gly Gly Gly Trp
            100                 105                 110
```

-continued

```
Val Ile Gly Asn Ala Gln Met Asn Asp Asp Leu Asn Ile Gly Ile Val
        115                 120                 125

Asn Ala Cys Asn Val Ala Val Val Ser Val Asp Tyr Arg Leu Ala Leu
    130                 135                 140

Ser Thr Pro Val Glu Gly Leu Met Asp Asp Cys Phe Ser Ala Ala Cys
145                 150                 155                 160

Trp Leu Leu Gly Ser Asp Cys Lys Glu Phe Ala Gly Leu Pro Val Ile
                165                 170                 175

Val Val Gly Glu Ser Ala Gly Gly His Leu Ala Ala Ala Thr Leu Leu
            180                 185                 190

Lys Leu Lys Ala Arg Pro Asp Leu Leu Lys Arg Val Val Gly Thr Val
        195                 200                 205

Leu Tyr Tyr Gly Val Tyr Asp Leu Thr Gly Thr Lys Ser Val Arg Thr
    210                 215                 220

Ala Gly Pro Glu Thr Leu Val Leu Asp Gly Pro Gly Met Val Gly Ala
225                 230                 235                 240

Met Arg Leu Leu Ala Pro Asp Arg Thr Asp Glu Lys Arg Arg Glu Pro
                245                 250                 255

Pro Leu Ser Pro Leu Tyr Gly Asp Leu Thr Asp Leu Pro Pro Ala Leu
            260                 265                 270

Met Phe Val Gly Glu Leu Asp Pro Leu Leu Asp Asp Thr Leu Glu Met
        275                 280                 285

Ala Glu Arg Trp Lys Asn Ser Ala Asp Val Glu Met His Leu Leu Pro
    290                 295                 300

Glu Ser Pro His Gly Phe Ile His Phe Pro Thr Ala Leu Ala Arg Lys
305                 310                 315                 320

Val Leu Ala Arg Ser His Glu Trp Ile Asn Ala Arg Met Glu Gly Arg
                325                 330                 335
Pro
```

<210> SEQ ID NO 17
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 17

```
atgcaaacct atatacccta tccaaaaaac cctcccaccg ttggtacagt tctgctgact     60

tcctatggct cattcgccca tgaaaacgag atacctaaat cttgtgctgc cgacgcttta    120

agagtaggca aagagctcgc tgatggtttc gatggcgagg ttcatcatct aggcgctctg    180

atgctgatga tttccgactt tccagcagag ccgctgctga aagcatctgc tgctaagaaa    240

ggttctttgc taggaattac ttcgcttggc tacctattat cctatggatc tactggtgaa    300

aaagcgaagc gaatcatcga agcaggttgt ggtatttttc tcgtcagagt gagtggtgat    360

attgaaaacc ctaaagcaaa aattgaagtt tatagctctt ggtctgaata ccagaagttc    420

cttgaaccca ttttgaagac aggtgacttt tatccagtga aaacgtcgtc gttttccgaa    480

taa                                                                  483
```

<210> SEQ ID NO 18
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 18

Met Gln Thr Tyr Ile Pro Tyr Pro Lys Asn Pro Pro Thr Val Gly Thr
1 5 10 15

Val Leu Leu Thr Ser Tyr Gly Ser Phe Ala His Glu Asn Glu Ile Pro
20 25 30

Lys Ser Cys Ala Ala Asp Ala Leu Arg Val Gly Lys Glu Leu Ala Asp
35 40 45

Gly Phe Asp Gly Glu Val His His Leu Gly Ala Leu Met Leu Met Ile
50 55 60

Ser Asp Phe Pro Ala Glu Pro Leu Leu Lys Ala Ser Ala Ala Lys Lys
65 70 75 80

Gly Ser Leu Leu Gly Ile Thr Ser Leu Gly Tyr Leu Leu Ser Tyr Gly
85 90 95

Ser Thr Gly Glu Lys Ala Lys Arg Ile Ile Glu Ala Gly Cys Gly Ile
100 105 110

Phe Leu Val Arg Val Ser Gly Asp Ile Glu Asn Pro Lys Ala Lys Ile
115 120 125

Glu Val Tyr Ser Ser Trp Ser Glu Tyr Gln Lys Phe Leu Glu Pro Ile
130 135 140

Leu Lys Thr Gly Asp Phe Tyr Pro Val Lys Thr Ser Ser Phe Ser Glu
145 150 155 160

<210> SEQ ID NO 19
<211> LENGTH: 1467
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 19

atgatcaacc tcacccacat tgcgtcttca ttggcgcggg cagcgctcag cgattcgaca 60

aagccgaaga tggagcgcgc gataaacgtc gcgagccaca tcgctggcaa agtcgcgttg 120

caggtcacca gctcattact ggagcagaaa ggtctgctta acgagcgtca gcagaaaggg 180

ctctcgatga ttctgaaggc cttgagcggc aaggagccgg tgaacaatgt cgagacgcac 240

gaagggggag gccgattcaa tctggcgcga gccgccttcg acgtggccag cgttgtctgg 300

gagcgcgaca agtcgatgca taacgtgatg agctttctgg gcgtcagcga cagcaagggc 360

aagatgttgt tctctctggg caagaagctg gcggatgcaa tggccaagcc tgagcctggc 420

aaggacaaca gtgaggccac aaatgcgcgc catgcctatt tctccagcaa cttgaaactg 480

aacaagttga tgaacgacct cactgaccag gttttcaaca agattcgcca gtcgaacggt 540

gatcgcgtgc gacgacccat gccagaacca ttctggagac cttacggcgc ccaacagcaa 600

gcgcgcccgc aaacgcctcc cggcactcgc ccacaagcca acagcgcccc gccaccgccg 660

ccgaaagcag agccacgacc tgcgtcgggc cggcctgacg gcgcccaaca gcaggcgcgc 720

ccggaaacgc cgcctcgtac tcgaccgcag gccaatagca ctccgccacc gccgccgaaa 780

gcagagccac gacctgcgtc gggccggcct gacggcgccc agcagcaagc acgcccggaa 840

acgccgccgc gcactcgccc gcaggcgaac agcacgccgc caccgccgcc caaggcagag 900

ccacgacctg cgtccggccg gcctgacggc gcccaacagc aagcacgccc ggaaacgcca 960

cctcgcactc gcccccaagc gaacagcgcg ccgcctccgc cgcccaaagc agagccacga 1020

cctgcgtccg gccggcctga cggcacccaa cagcaagcac gcccggaaac gccacctcgc 1080

actcgccccc aagcgaacag cgcgccgcct ccgccgccca aagcagaacc cagcgcaggc 1140

ggcgaacggc cttcaacggc gcggcccaat aacacatcgg ctgctgacgc atctgccagg 1200

-continued

gtgggcgatt ccgcacctgc caagccgccc gtcaagccgt tgtacgagca cttgggcctc 1260

actgacatgt cggtagactt atccgccgtt aaaaaggctt acagagatgc cgcgatgaag 1320

aaccaccctg ataaaaaccg cggcaacgag gccgaggcgg ccgagcgctt caaagtcatt 1380

tcaaatgcgt acaagatttt gtccgacccg gagttgcgca aagcatacga caacggccgt 1440

atcaatgagg ctggtaatag ggcatga 1467

<210> SEQ ID NO 20
<211> LENGTH: 488
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 20

Met Ile Asn Leu Thr His Ile Ala Ser Ser Leu Ala Arg Ala Ala Leu
1 5 10 15

Ser Asp Ser Thr Lys Pro Lys Met Glu Arg Ala Ile Asn Val Ala Ser
20 25 30

His Ile Ala Gly Lys Val Ala Leu Gln Val Thr Ser Ser Leu Leu Glu
35 40 45

Gln Lys Gly Leu Leu Asn Glu Arg Gln Gln Lys Gly Leu Ser Met Ile
50 55 60

Leu Lys Ala Leu Ser Gly Lys Glu Pro Val Asn Asn Val Glu Thr His
65 70 75 80

Glu Gly Gly Gly Arg Phe Asn Leu Ala Arg Ala Ala Phe Asp Val Ala
85 90 95

Ser Val Val Trp Glu Arg Asp Lys Ser Met His Asn Val Met Ser Phe
100 105 110

Leu Gly Val Ser Asp Ser Lys Gly Lys Met Leu Phe Ser Leu Gly Lys
115 120 125

Lys Leu Ala Asp Ala Met Ala Lys Pro Glu Pro Gly Lys Asp Asn Ser
130 135 140

Glu Ala Thr Asn Ala Arg His Ala Tyr Phe Ser Ser Asn Leu Lys Leu
145 150 155 160

Asn Lys Leu Met Asn Asp Leu Thr Asp Gln Val Phe Asn Lys Ile Arg
165 170 175

Gln Ser Asn Gly Asp Arg Val Arg Arg Pro Met Pro Glu Pro Phe Trp
180 185 190

Arg Pro Tyr Gly Ala Gln Gln Gln Ala Arg Pro Gln Thr Pro Pro Gly
195 200 205

Thr Arg Pro Gln Ala Asn Ser Ala Pro Pro Pro Pro Pro Lys Ala Glu
210 215 220

Pro Arg Pro Ala Ser Gly Arg Pro Asp Gly Ala Gln Gln Gln Ala Arg
225 230 235 240

Pro Glu Thr Pro Pro Arg Thr Arg Pro Gln Ala Asn Ser Thr Pro Pro
245 250 255

Pro Pro Pro Lys Ala Glu Pro Arg Pro Ala Ser Gly Arg Pro Asp Gly
260 265 270

Ala Gln Gln Gln Ala Arg Pro Glu Thr Pro Pro Arg Thr Arg Pro Gln
275 280 285

Ala Asn Ser Thr Pro Pro Pro Pro Pro Lys Ala Glu Pro Arg Pro Ala
290 295 300

Ser Gly Arg Pro Asp Gly Ala Gln Gln Gln Ala Arg Pro Glu Thr Pro
305 310 315 320

-continued

```
Pro Arg Thr Arg Pro Gln Ala Asn Ser Ala Pro Pro Pro Pro Pro Lys
                325                 330                 335

Ala Glu Pro Arg Pro Ala Ser Gly Arg Pro Asp Gly Thr Gln Gln Gln
            340                 345                 350

Ala Arg Pro Glu Thr Pro Pro Arg Thr Arg Pro Gln Ala Asn Ser Ala
        355                 360                 365

Pro Pro Pro Pro Pro Lys Ala Glu Pro Ser Ala Gly Gly Glu Arg Pro
    370                 375                 380

Ser Thr Ala Arg Pro Asn Asn Thr Ser Ala Ala Asp Ala Ser Ala Arg
385                 390                 395                 400

Val Gly Asp Ser Ala Pro Ala Lys Pro Pro Val Lys Pro Leu Tyr Glu
                405                 410                 415

His Leu Gly Leu Thr Asp Met Ser Val Asp Leu Ser Ala Val Lys Lys
            420                 425                 430

Ala Tyr Arg Asp Ala Ala Met Lys Asn His Pro Asp Lys Asn Arg Gly
        435                 440                 445

Asn Glu Ala Glu Ala Ala Glu Arg Phe Lys Val Ile Ser Asn Ala Tyr
    450                 455                 460

Lys Ile Leu Ser Asp Pro Glu Leu Arg Lys Ala Tyr Asp Asn Gly Arg
465                 470                 475                 480

Ile Asn Glu Ala Gly Asn Arg Ala
                485
```

<210> SEQ ID NO 21
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 21

```
atgaacatta cgccgctcac gtcagccgcg ggcaagggct cgtccgcaca aggcacagac     60

aaaatttcca ttcccaactc cacgcgcatg atcaatgccg cttcaatcaa gtggttgaat    120

aaggtgcgta gcgccatcag tgaccacatc cgcaccagca tcgagaaagg gaaactgttc    180

gagctcgcct ccttgggcag caacatgttc ggtgtcccgg ctctttcagc gcgcccctcg    240

acgctccaac ctgtgttggc gtttgaggct gaccccaatc acgacctgaa ccttgtcagg    300

gtctatatgc aggacagcgc cggcaagctc actccctggg acccgacgcc caacgcggtc    360

acgacgacgt cgaatccatc agagcctgat gcgcagagcg atacggcttc gtcatcatta    420

cctcggcggc ctcccgcagg ctcggtgctg agtttgctgg gcattgcgct ggatcacgcg    480

caacgccaca gtcctcgcgc ggacaggtct gccaagggac gacctggccg agaggagagg    540

aacggggcaa ggttcaatgc caagcaaaca aagccgacag aggctgaagc ctacggtgat    600

catcagacac ccaatcctga tttgcacagg caaaaagaga cagctcaacg cgttgctgaa    660

agcatcaaca gcatgcgaga gcagcaaaat ggaatgcaac gcgccgaagg gcttctcaga    720

gccaaagaag cgttgcaagc tcgggaagcc gcgcgcaagc agcttctgga cgtgctcgag    780

gccatccagg ctggccgtga agactccacc gacaagaaga tcagcgccac tgaaaagaac    840

gccacgggca tcaactacca gtga                                           864
```

<210> SEQ ID NO 22
<211> LENGTH: 287
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 22

Met Asn Ile Thr Pro Leu Thr Ser Ala Ala Gly Lys Gly Ser Ser Ala
1 5 10 15

Gln Gly Thr Asp Lys Ile Ser Ile Pro Asn Ser Thr Arg Met Ile Asn
20 25 30

Ala Ala Ser Ile Lys Trp Leu Asn Lys Val Arg Ser Ala Ile Ser Asp
35 40 45

His Ile Arg Thr Ser Ile Glu Lys Gly Lys Leu Phe Glu Leu Ala Ser
50 55 60

Leu Gly Ser Asn Met Phe Gly Val Pro Ala Leu Ser Ala Arg Pro Ser
65 70 75 80

Thr Leu Gln Pro Val Leu Ala Phe Glu Ala Asp Pro Asn His Asp Leu
85 90 95

Asn Leu Val Arg Val Tyr Met Gln Asp Ser Ala Gly Lys Leu Thr Pro
100 105 110

Trp Asp Pro Thr Pro Asn Ala Val Thr Thr Thr Ser Asn Pro Ser Glu
115 120 125

Pro Asp Ala Gln Ser Asp Thr Ala Ser Ser Ser Leu Pro Arg Arg Pro
130 135 140

Pro Ala Gly Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Asp His Ala
145 150 155 160

Gln Arg His Ser Pro Arg Ala Asp Arg Ser Ala Lys Gly Arg Pro Gly
165 170 175

Arg Glu Glu Arg Asn Gly Ala Arg Phe Asn Ala Lys Gln Thr Lys Pro
180 185 190

Thr Glu Ala Glu Ala Tyr Gly Asp His Gln Thr Pro Asn Pro Asp Leu
195 200 205

His Arg Gln Lys Glu Thr Ala Gln Arg Val Ala Glu Ser Ile Asn Ser
210 215 220

Met Arg Glu Gln Gln Asn Gly Met Gln Arg Ala Glu Gly Leu Leu Arg
225 230 235 240

Ala Lys Glu Ala Leu Gln Ala Arg Glu Ala Ala Arg Lys Gln Leu Leu
245 250 255

Asp Val Leu Glu Ala Ile Gln Ala Gly Arg Glu Asp Ser Thr Asp Lys
260 265 270

Lys Ile Ser Ala Thr Glu Lys Asn Ala Thr Gly Ile Asn Tyr Gln
275 280 285

<210> SEQ ID NO 23
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 23

atgcgcacat ccgttaatgg tctgcttgag cacagcctga agaccctggg ctttgatact 60

tcggcattgc aggccttgcg cgacgacggt tatttactgt ggcaaggcaa ggataagcaa 120

gccagtcttc tggttccctc tactgacggc gacgcgcttt tcgctatctg taccttgagc 180

cgtgtcgatc ccgagcacga cggacgtctg ctggcgcttg cattgcacct gaacctgtct 240

cctgtccaca cgatgagcgc atgtatagca cttgatgtcg agcaaaacac gttgtgtctt 300

cgctacaccc atgaccttgg cgggaacggg gcagataccc tgttgcttgc gctcgaaaac 360

gcccaagcgc ttgctgaaca gatcaagcag gtaatcgaaa actttaggca cgatcaggga 420

cgccgatag 429

-continued

<210> SEQ ID NO 24
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 24

Met Arg Thr Ser Val Asn Gly Leu Leu Glu His Ser Leu Lys Thr Leu
1 5 10 15

Gly Phe Asp Thr Ser Ala Leu Gln Ala Leu Arg Asp Asp Gly Tyr Leu
20 25 30

Leu Trp Gln Gly Lys Asp Lys Gln Ala Ser Leu Leu Val Pro Ser Thr
35 40 45

Asp Gly Asp Ala Leu Phe Ala Ile Cys Thr Leu Ser Arg Val Asp Pro
50 55 60

Glu His Asp Gly Arg Leu Leu Ala Leu Ala Leu His Leu Asn Leu Ser
65 70 75 80

Pro Val His Thr Met Ser Ala Cys Ile Ala Leu Asp Val Glu Gln Asn
85 90 95

Thr Leu Cys Leu Arg Tyr Thr His Asp Leu Gly Gly Asn Gly Ala Asp
100 105 110

Thr Leu Leu Leu Ala Leu Glu Asn Ala Gln Ala Leu Ala Glu Gln Ile
115 120 125

Lys Gln Val Ile Glu Asn Phe Arg His Asp Gln Gly Arg Arg
130 135 140

<210> SEQ ID NO 25
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 25

atgatcgcgt tcgcaaccgg actgctagaa cacagcctga aacggcttgg atacgacgcc 60

gcagatttgc aatcccttcg ggatgaaggg tatttgctgt ggcacgggaa aaacggtcac 120

accagcctgt tggtgcccgc tgctggcggg gatgcgcttt ttgtcatcag caccctgagc 180

tacatcgatc ctgaacagga cgggcggctg ctggcgcttg cgctgcattt gaacttgtcg 240

ccagcccaca ctctgggcgc cagtatcgcg ctggatatcg agcaaaatac cttgtgcctg 300

cgttacacgc acgacctcac tgggcacggc acagacaatt tgtcccgcgc gcttgaaagc 360

actcaggcac ttgccgagca gatcaagcag gtcatcgaaa ccttccgcag tgaattcgga 420

cgcccgccaa tgcccgccca cacagcccga cggccagatg ccgtggcgct ttag 474

<210> SEQ ID NO 26
<211> LENGTH: 157
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 26

Met Ile Ala Phe Ala Thr Gly Leu Leu Glu His Ser Leu Lys Arg Leu
1 5 10 15

Gly Tyr Asp Ala Ala Asp Leu Gln Ser Leu Arg Asp Glu Gly Tyr Leu
20 25 30

Leu Trp His Gly Lys Asn Gly His Thr Ser Leu Leu Val Pro Ala Ala
35 40 45

Gly Gly Asp Ala Leu Phe Val Ile Ser Thr Leu Ser Tyr Ile Asp Pro
50 55 60

-continued

```
Glu Gln Asp Gly Arg Leu Leu Ala Leu Ala Leu His Leu Asn Leu Ser
 65                  70                  75                  80

Pro Ala His Thr Leu Gly Ala Ser Ile Ala Leu Asp Ile Glu Gln Asn
                 85                  90                  95

Thr Leu Cys Leu Arg Tyr Thr His Asp Leu Thr Gly His Gly Thr Asp
            100                 105                 110

Asn Leu Ser Arg Ala Leu Glu Ser Thr Gln Ala Leu Ala Glu Gln Ile
        115                 120                 125

Lys Gln Val Ile Glu Thr Phe Arg Ser Glu Phe Gly Arg Pro Pro Met
    130                 135                 140

Pro Ala His Thr Ala Arg Arg Pro Asp Ala Val Ala Leu
145                 150                 155


<210> SEQ ID NO 27
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 27

gtgaaaaagt ctggcgctgg aactcaagcc tatgcgttgt tcgcctctgc gacgggaagc     60

tcgtcgaagg gcgttctaag taccattgcc aggcacctga cgggatgttt tgcacccaac    120

aagactgcgc ttcattcagc aacagccgtt tcgtatgagc tattgccggg caattattct    180

gtcgccgcca gtgtgcatgg cttgtcggtt gatcaccgcc agccggcgct gacacgactg    240

agtaacgtgc tgttcaatca ggcactggcg ctggacctgg agcgttttga cgagggcgcg    300

ccagccgacg aaatgttcag gccttcactg aaacgcgaag gtgcccatcc ccgattggcc    360

gactcactgg gtggcgagca actggctgtg caaaccatgg agaagggcct taaacggctg    420

gcagaggatc ctgcgcagtc ctttgcgcga tgccattcat ttttttaccc gatcagtagt    480

gataccactt cacctcaagc atcacttcat tctgtggcga gctcatctgg ctga          534


<210> SEQ ID NO 28
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 28

Val Lys Lys Ser Gly Ala Gly Thr Gln Ala Tyr Ala Leu Phe Ala Ser
  1               5                  10                  15

Ala Thr Gly Ser Ser Ser Lys Gly Val Leu Ser Thr Ile Ala Arg His
             20                  25                  30

Leu Thr Gly Cys Phe Ala Pro Asn Lys Thr Ala Leu His Ser Ala Thr
         35                  40                  45

Ala Val Ser Tyr Glu Leu Leu Pro Gly Asn Tyr Ser Val Ala Ala Ser
     50                  55                  60

Val His Gly Leu Ser Val Asp His Arg Gln Pro Ala Leu Thr Arg Leu
 65                  70                  75                  80

Ser Asn Val Leu Phe Asn Gln Ala Leu Ala Leu Asp Leu Glu Arg Phe
                 85                  90                  95

Asp Glu Gly Ala Pro Ala Asp Glu Met Phe Arg Pro Ser Leu Lys Arg
            100                 105                 110

Glu Gly Ala His Pro Arg Leu Ala Asp Ser Leu Gly Gly Glu Gln Leu
        115                 120                 125

Ala Val Gln Thr Met Glu Lys Gly Leu Lys Arg Leu Ala Glu Asp Pro
    130                 135                 140
```

-continued

```
Ala Gln Ser Phe Ala Arg Cys His Ser Phe Phe Tyr Pro Ile Ser Ser
145                 150                 155                 160

Asp Thr Thr Ser Pro Gln Ala Ser Leu His Ser Val Ala Ser Ser Ser
                165                 170                 175
Gly
```

<210> SEQ ID NO 29
<211> LENGTH: 1137
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 29

```
atgaaaacag tcagcaatca ctcgataccc agtacaaatc tcgtcgtgga tgcgggaacg     60

gaaacttcgg cgcagaaatc ccagccggtt tgcagcgaaa tccagcgtaa cagcaagatc    120

gaaaaagcag tcatcgaaca cattgccgac cacccggcag cgaaaatgac aataagcgcg    180

ctggttgaca cgttgacaga cgtttttgtc agggctcatg gggaggttaa ggggtgggcc    240

gaaatcgtcc aggcagtctc tcgccctcat gacagtaatc gacacggcag tggagtgctc    300

agcccgcgct ttgatgtaat ggggagtgtt ggttggaatg cggcagctat ccgggccacc    360

agtcgcgtcg ggacgcttcg agagaaaggt acactgttca ctaaccttat gctcagtaac    420

aactttaaac atttgcttaa acgagtggtt aacgatccag ccttgcagca aaagctcgac    480

ggtgggttag acctcaacta tctgaaggct tgtgaaggcg atctttatgt catgtcaggg    540

tgggctgcac gggctagcga aagtcgtgaa caaattggca aagcccggta tgaaacggca    600

tcaaatctta gccagacgct gatcagtgca cgtgagttgg cttttcatcg tcacaatccg    660

gttaatcatc cgtctgccca aacgaaagtg ggcttcgata agggtttgcc tgaggaatct    720

gatctgcagg ttctgagagg ccatggcagc agtgtatgga gtgtaaaacc gggcagcgat    780

ttcgcaaagc gtgctgaagt ttctggaaag cctattatcg ccggcccgtc cggtaccgct    840

tcgcgcatgg tcgctgttgc gcgttttctg gcaccggctt gtttgaaaag cctgggtatt    900

gagagtgagc agaacctgaa agagcttgtg cggtatgcct gctatgccta tttcggtcag    960

gacagccacc attcgatgct tgaagtgaat cttggtgtcg cttcccatgg aatgccggaa   1020

caatgggacg acacgcttta taacgagcct ttcagtaatt caattaaagg tcgcgggttt   1080

ggtatagaca atctcgcgca taggcaagtc gtcaggcagg cggctcaaaa gtcatga      1137
```

<210> SEQ ID NO 30
<211> LENGTH: 378
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 30

```
Met Lys Thr Val Ser Asn His Ser Ile Pro Ser Thr Asn Leu Val Val
  1               5                  10                  15

Asp Ala Gly Thr Glu Thr Ser Ala Gln Lys Ser Gln Pro Val Cys Ser
             20                  25                  30

Glu Ile Gln Arg Asn Ser Lys Ile Glu Lys Ala Val Ile Glu His Ile
         35                  40                  45

Ala Asp His Pro Ala Ala Lys Met Thr Ile Ser Ala Leu Val Asp Thr
     50                  55                  60

Leu Thr Asp Val Phe Val Arg Ala His Gly Glu Val Lys Gly Trp Ala
 65                  70                  75                  80

Glu Ile Val Gln Ala Val Ser Arg Pro His Asp Ser Asn Arg His Gly
                 85                  90                  95
```

-continued

```
Ser Gly Val Leu Ser Pro Arg Phe Asp Val Met Gly Ser Val Gly Trp
            100                 105                 110

Asn Ala Ala Ala Ile Arg Ala Thr Ser Arg Val Gly Thr Leu Arg Glu
        115                 120                 125

Lys Gly Thr Leu Phe Thr Asn Leu Met Leu Ser Asn Asn Phe Lys His
    130                 135                 140

Leu Leu Lys Arg Val Val Asn Asp Pro Ala Leu Gln Gln Lys Leu Asp
145                 150                 155                 160

Gly Gly Leu Asp Leu Asn Tyr Leu Lys Ala Cys Glu Gly Asp Leu Tyr
                165                 170                 175

Val Met Ser Gly Trp Ala Ala Arg Ala Ser Glu Ser Arg Glu Gln Ile
            180                 185                 190

Gly Lys Ala Arg Tyr Glu Thr Ala Ser Asn Leu Ser Gln Thr Leu Ile
        195                 200                 205

Ser Ala Arg Glu Leu Ala Phe His Arg His Asn Pro Val Asn His Pro
    210                 215                 220

Ser Ala Gln Thr Lys Val Gly Phe Asp Lys Gly Leu Pro Glu Glu Ser
225                 230                 235                 240

Asp Leu Gln Val Leu Arg Gly His Gly Ser Ser Val Trp Ser Val Lys
                245                 250                 255

Pro Gly Ser Asp Phe Ala Lys Arg Ala Glu Val Ser Gly Lys Pro Ile
            260                 265                 270

Ile Ala Gly Pro Ser Gly Thr Ala Ser Arg Met Val Ala Val Ala Arg
        275                 280                 285

Phe Leu Ala Pro Ala Cys Leu Lys Ser Leu Gly Ile Glu Ser Glu Gln
    290                 295                 300

Asn Leu Lys Glu Leu Val Arg Tyr Ala Cys Tyr Ala Tyr Phe Gly Gln
305                 310                 315                 320

Asp Ser His His Ser Met Leu Glu Val Asn Leu Gly Val Ala Ser His
                325                 330                 335

Gly Met Pro Glu Gln Trp Asp Asp Thr Leu Tyr Asn Glu Pro Phe Ser
            340                 345                 350

Asn Ser Ile Lys Gly Arg Gly Phe Gly Ile Asp Asn Leu Ala His Arg
        355                 360                 365

Gln Val Val Arg Gln Ala Ala Gln Lys Ser
    370                 375
```

<210> SEQ ID NO 31
<211> LENGTH: 1173
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 31

```
atgcggtttg atgctgcccg aggccagaag cccaaagccc ctatggatgc accgtcatca     60

ttacgtttgc gagcgatagc aggtggcatg cccagtgaag aagcaggaac gactgcacct    120

gctgacgtga atcagcctcc acctgctgat gttcgtccag aaatgggtgt aggtcctgtg    180

agactcttcg ttaaactgat ggtaggaact ctggcgctgt cgacaggagt ccgttttgca    240

agatacccag gtgatttcgc gaaggatccg ggaggcagtg tatgggcagc aatcaatctg    300

cagcatcgct cgagcgtcac acatcttgaa caaggcaata agacggttct tgagcgtttc    360

ggtgcacata ttccaaaaga cagtgcgtgt ttcaaagctc gcgctgacgt cacacacgat    420

gttccctcag gcgtggcagg gcagtggaac cacaaaaccc aacgggtaaa actgaaccct    480

aacattcatt tcgagagcca tccggcacag gtcgccggac atgagttcat acactgttac    540
```

-continued

```
acgcatcctg agtttgtcga acgccatata aaacatccgc actggaaagc cctgaacgaa    600

gggttgacga ctcgtttgac agagaaactg ccagacccta agcgtctctt gcccattccc    660

ttggcaaagg atccctatca tggtttcaag ctgtccaccg gggactcctg gccggatgcg    720

gccaggcgaa tcgaagacga agttggcgaa gatgtgttgt tgaaagcgtt ctttggcggc    780

gatgaccagg ctattagtga agtagctaaa gccgctgctc agatctaccc caagattgcc    840

tcacgtatta ccgagaggga gttgtatcaa gcgggcagca tgcgtggagg acaacagctg    900

gccgagtgtt acgtaggtgc tttgctcaaa aacggtcaga aactgcctga cagttttacg    960

aattatctgc tacctgtatt tagctattca gatataagcc ctggtcacgc gaaaaaaata   1020

caggcgcaag cggaaaaaag tcaaaagcgg atgggaattg tgttcgatac agcgtttttt   1080

tcacctgacc tgaagaccca gagactggca cttggcatgc tacgggagga cctgctgatg   1140

cactggaaaa aagttattcc ggatagaaag taa                                1173
```

<210> SEQ ID NO 32
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 32

```
Met Arg Phe Asp Ala Ala Arg Gly Gln Lys Pro Lys Ala Pro Met Asp
  1               5                  10                  15

Ala Pro Ser Ser Leu Arg Leu Arg Ala Ile Ala Gly Gly Met Pro Ser
             20                  25                  30

Glu Glu Ala Gly Thr Thr Ala Pro Ala Asp Val Asn Gln Pro Pro Pro
         35                  40                  45

Ala Asp Val Arg Pro Glu Met Gly Val Gly Pro Val Arg Leu Phe Val
     50                  55                  60

Lys Leu Met Val Gly Thr Leu Ala Leu Ser Thr Gly Val Arg Phe Ala
 65                  70                  75                  80

Arg Tyr Pro Gly Asp Phe Ala Lys Asp Pro Gly Gly Ser Val Trp Ala
                 85                  90                  95

Ala Ile Asn Leu Gln His Arg Ser Ser Val Thr His Leu Glu Gln Gly
            100                 105                 110

Asn Lys Thr Val Leu Glu Arg Phe Gly Ala His Ile Pro Lys Asp Ser
        115                 120                 125

Ala Cys Phe Lys Ala Arg Ala Asp Val Thr His Asp Val Pro Ser Gly
    130                 135                 140

Val Ala Gly Gln Trp Asn His Lys Thr Gln Arg Val Lys Leu Asn Pro
145                 150                 155                 160

Asn Ile His Phe Glu Ser His Pro Ala Gln Val Ala Gly His Glu Phe
                165                 170                 175

Ile His Cys Tyr Thr His Pro Glu Phe Val Glu Arg His Ile Lys His
            180                 185                 190

Pro His Trp Lys Ala Leu Asn Glu Gly Leu Thr Thr Arg Leu Thr Glu
        195                 200                 205

Lys Leu Pro Asp Pro Lys Arg Leu Leu Pro Ile Pro Leu Ala Lys Asp
    210                 215                 220

Pro Tyr His Gly Phe Lys Leu Ser Thr Gly Asp Ser Trp Pro Asp Ala
225                 230                 235                 240

Ala Arg Arg Ile Glu Asp Glu Val Gly Glu Asp Val Leu Leu Lys Ala
                245                 250                 255
```

-continued

```
Phe Phe Gly Gly Asp Asp Gln Ala Ile Ser Glu Val Ala Lys Ala Ala
            260                 265                 270

Ala Gln Ile Tyr Pro Lys Ile Ala Ser Arg Ile Thr Glu Arg Glu Leu
        275                 280                 285

Tyr Gln Ala Gly Ser Met Arg Gly Gly Gln Gln Leu Ala Glu Cys Tyr
    290                 295                 300

Val Gly Ala Leu Leu Lys Asn Gly Gln Lys Leu Pro Asp Ser Phe Thr
305                 310                 315                 320

Asn Tyr Leu Leu Pro Val Phe Ser Tyr Ser Asp Ile Ser Pro Gly His
                325                 330                 335

Ala Lys Lys Ile Gln Ala Gln Ala Glu Lys Ser Gln Lys Arg Met Gly
            340                 345                 350

Ile Val Phe Asp Thr Ala Phe Phe Ser Pro Asp Leu Lys Thr Gln Arg
        355                 360                 365

Leu Ala Leu Gly Met Leu Arg Glu Asp Leu Leu Met His Trp Lys Lys
    370                 375                 380

Val Ile Pro Asp Arg Lys
385                 390


<210> SEQ ID NO 33
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 33

atgaacaggc ttcacaagac cagtctgctg gcggctatat tgaccgcatc cccctgcatt     60

atggcagcta acgctcatgc tatgagttgt cctgtcccgc aaagcgtgaa gtacgttaat    120

ggtatctata tcgcgccgga aacgtttgct ggttgggagg ggaactgggt ttctcaacca    180

cacaagaaac actccattaa agagttttcc actgctttat atctttcagt ggataaaagt    240

cagaagggag gaacattgac taactgtagt tattcactaa gcggagataa tggcgtaata    300

gatcttgagt atcgaaaatc aggaaatgag aatagactaa agacacttat cgtttccatt    360

gaaggtcagc acaattggat taaagagcgt ggcgcggttg gaattcaagg atatgaatgt    420

acaaagtcag catctgagtg tcagttcgtt ccgctgcggc taaacgagga ctga          474


<210> SEQ ID NO 34
<211> LENGTH: 157
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 34

Met Asn Arg Leu His Lys Thr Ser Leu Leu Ala Ala Ile Leu Thr Ala
  1               5                  10                  15

Ser Pro Cys Ile Met Ala Ala Asn Ala His Ala Met Ser Cys Pro Val
             20                  25                  30

Pro Gln Ser Val Lys Tyr Val Asn Gly Ile Tyr Ile Ala Pro Glu Thr
         35                  40                  45

Phe Ala Gly Trp Glu Gly Asn Trp Val Ser Gln Pro His Lys Lys His
     50                  55                  60

Ser Ile Lys Glu Phe Ser Thr Ala Leu Tyr Leu Ser Val Asp Lys Ser
 65                  70                  75                  80

Gln Lys Gly Gly Thr Leu Thr Asn Cys Ser Tyr Ser Leu Ser Gly Asp
                 85                  90                  95

Asn Gly Val Ile Asp Leu Glu Tyr Arg Lys Ser Gly Asn Glu Asn Arg
            100                 105                 110
```

-continued

```
Leu Lys Thr Leu Ile Val Ser Ile Glu Gly Gln His Asn Trp Ile Lys
        115                 120                 125

Glu Arg Gly Ala Val Gly Ile Gln Gly Tyr Glu Cys Thr Lys Ser Ala
    130                 135                 140

Ser Glu Cys Gln Phe Val Pro Leu Arg Leu Asn Glu Asp
145                 150                 155
```

<210> SEQ ID NO 35
<211> LENGTH: 1344
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 35

```
atgcatcgtc ctatcaccgc aggccatacc acctcacgtc tcatcctaga tcagtcaaaa     60

caaatatcac gtaccccatc ggaaagtagc gcgcaatcag cgctttctca gcaagcaagc    120

atgagcagcc cagttttgga gcggtcgaaa agtgcgccag ctttattgac tgcggcacag    180

cgcacgatgc ttgcacaagt gggagcctgt aacgctcatc tgacctcaga tgaaaacatg    240

gccatcaacg aactgagatc acacaagccc cttttaccta aggatacgtg gtttttcact    300

gatcctaaca aggacccaga tgatgtcgtg acctacacct tgggcaagca attgcaggct    360

gagggctttg tgcacatcac ggatgtagtg gcgacactgg gtgatgctga agttcgctct    420

caacgtgccg agatggccaa aggcgtgttc aacaagcttg agttgcatga cgtgcatgtg    480

tcgcgtggtc gggattacgc aatgaattcg cttcagtcga aggaacatgc caaattttta    540

ctggaaggtc atgctttaag ggctggacct ggtgaaatac accgcgacag cttgcaggac    600

atgagcaggc gcctggcccg tgcgccacat ggagtcggta ttgtcgtaat tgcaggcatg    660

agtgatatca atgcgctcat cactacctgc ccggatatgg tgcgcgaacg ggttgatgac    720

atcaccatca tgggcggcgt cgagccttta aaggacgcag atggttttgt acagcctgat    780

gcacgcgctt acaacaatgc gaccgacatg gacgctgcgc gcagtcttta tcggaaagcg    840

caggagcttg gcattccact tcgtatagtg acaaaggagg cggcctataa aacggcggtt    900

tcgccttcat tttacgaagg gatagcgggg agcggacatc cagtaggcca ctacctgaga    960

gacgttcaga agagtgcgtt gaaaggcctc tgggaaggta ttcaagctgg attgcttccc   1020

gggttggatg actcatggtt ctttcggacg ttcatgccga atgcacagat tgaagcagca   1080

caactggata aaaataaaga gagttcgttt gaagatatct ggcctaaggt gacgaagcta   1140

aacctgtatg atcctctgac attactggcc tcagtgccag gggcggcaaa actgctattt   1200

aaaccaaaag ctatacacac agaaggattt ggtgttgtag agcaagtagg tccagatgat   1260

gtgacgcatc cagagaaagc aaagttattg atgtccgctt tagccaaatc tgcgcttgtc   1320

cagtcgacgg tagccccaga ttga                                          1344
```

<210> SEQ ID NO 36
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 36

```
Met His Arg Pro Ile Thr Ala Gly His Thr Thr Ser Arg Leu Ile Leu
  1               5                  10                  15

Asp Gln Ser Lys Gln Ile Ser Arg Thr Pro Ser Glu Ser Ser Ala Gln
             20                  25                  30

Ser Ala Leu Ser Gln Gln Ala Ser Met Ser Ser Pro Val Leu Glu Arg
         35                  40                  45
```

-continued

```
Ser Lys Ser Ala Pro Ala Leu Leu Thr Ala Ala Gln Arg Thr Met Leu
     50                  55                  60

Ala Gln Val Gly Ala Cys Asn Ala His Leu Thr Ser Asp Glu Asn Met
 65                  70                  75                  80

Ala Ile Asn Glu Leu Arg Ser His Lys Pro Leu Leu Pro Lys Asp Thr
                 85                  90                  95

Trp Phe Phe Thr Asp Pro Asn Lys Asp Pro Asp Asp Val Val Thr Tyr
            100                 105                 110

Thr Leu Gly Lys Gln Leu Gln Ala Glu Gly Phe Val His Ile Thr Asp
        115                 120                 125

Val Val Ala Thr Leu Gly Asp Ala Glu Val Arg Ser Gln Arg Ala Glu
    130                 135                 140

Met Ala Lys Gly Val Phe Asn Lys Leu Glu Leu His Asp Val His Val
145                 150                 155                 160

Ser Arg Gly Arg Asp Tyr Ala Met Asn Ser Leu Gln Ser Lys Glu His
                165                 170                 175

Ala Lys Phe Leu Leu Glu Gly His Ala Leu Arg Ala Gly Pro Gly Glu
            180                 185                 190

Ile His Arg Asp Ser Leu Gln Asp Met Ser Arg Arg Leu Ala Arg Ala
        195                 200                 205

Pro His Gly Val Gly Ile Val Val Ile Ala Gly Met Ser Asp Ile Asn
    210                 215                 220

Ala Leu Ile Thr Thr Cys Pro Asp Met Val Arg Glu Arg Val Asp Asp
225                 230                 235                 240

Ile Thr Ile Met Gly Gly Val Glu Pro Leu Lys Asp Ala Asp Gly Phe
                245                 250                 255

Val Gln Pro Asp Ala Arg Ala Tyr Asn Asn Ala Thr Asp Met Asp Ala
            260                 265                 270

Ala Arg Ser Leu Tyr Arg Lys Ala Gln Glu Leu Gly Ile Pro Leu Arg
        275                 280                 285

Ile Val Thr Lys Glu Ala Ala Tyr Lys Thr Ala Val Ser Pro Ser Phe
    290                 295                 300

Tyr Glu Gly Ile Ala Gly Ser Gly His Pro Val Gly His Tyr Leu Arg
305                 310                 315                 320

Asp Val Gln Lys Ser Ala Leu Lys Gly Leu Trp Glu Gly Ile Gln Ala
                325                 330                 335

Gly Leu Leu Pro Gly Leu Asp Asp Ser Trp Phe Phe Arg Thr Phe Met
            340                 345                 350

Pro Asn Ala Gln Ile Glu Ala Ala Gln Leu Asp Lys Asn Lys Glu Ser
        355                 360                 365

Ser Phe Glu Asp Ile Trp Pro Lys Val Thr Lys Leu Asn Leu Tyr Asp
    370                 375                 380

Pro Leu Thr Leu Leu Ala Ser Val Pro Gly Ala Ala Lys Leu Leu Phe
385                 390                 395                 400

Lys Pro Lys Ala Ile His Thr Glu Gly Phe Gly Val Val Glu Gln Val
                405                 410                 415

Gly Pro Asp Asp Val Thr His Pro Glu Lys Ala Lys Leu Leu Met Ser
            420                 425                 430

Ala Leu Ala Lys Ser Ala Leu Val Gln Ser Thr Val Ala Pro Asp
        435                 440                 445
```

-continued

<210> SEQ ID NO 37
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 37

gtgaaaatca atctccccgc gctcagaaca acgtcttcac gcgtgcagat ctgcttgacc 60

gcagtcctgc tgtgcacacc gctgctgttt tccgcgcatg cccaggcagc cggcacggct 120

tctgaacaag ccaatgtgga agtgatgatt cgtcagctca acgcgctcga ggccgtcgcc 180

cagcgcagtg tcgatcttcc acaagacccg gcccaacgct atcacctgga ctatccccgg 240

ttggtcagcg acatcgcgcg catccgccag ggcttgcaag actacctgtc gccgtcccgc 300

gcacagcccc gcgaccccgt ggagctatca ggccattaca acgtcagcgg tgatcacacg 360

ccatga 366

<210> SEQ ID NO 38
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 38

Val Lys Ile Asn Leu Pro Ala Leu Arg Thr Thr Ser Ser Arg Val Gln
1 5 10 15

Ile Cys Leu Thr Ala Val Leu Leu Cys Thr Pro Leu Leu Phe Ser Ala
20 25 30

His Ala Gln Ala Ala Gly Thr Ala Ser Glu Gln Ala Asn Val Glu Val
35 40 45

Met Ile Arg Gln Leu Asn Ala Leu Glu Ala Val Ala Gln Arg Ser Val
50 55 60

Asp Leu Pro Gln Asp Pro Ala Gln Arg Tyr His Leu Asp Tyr Pro Arg
65 70 75 80

Leu Val Ser Asp Ile Ala Arg Ile Arg Gln Gly Leu Gln Asp Tyr Leu
85 90 95

Ser Pro Ser Arg Ala Gln Pro Arg Asp Pro Val Glu Leu Ser Gly His
100 105 110

Tyr Asn Val Ser Gly Asp His Thr Pro
115 120

<210> SEQ ID NO 39
<211> LENGTH: 1242
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 39

atgcgttcca gggttataac tacatcgctg gtagtcatta tgctctcatg tgcatcagcc 60

gctccagctt gcttctccgc agacatgact cccagcgtgt cgaacgagag cacgtcggag 120

gcggattttc agcaatggct ggctactttc cgcagcaatg caactactaa gggcatcgac 180

acagccacac tcgatcttgc tttccaaaac atcacgcttg acccgactgt gcaccagttg 240

gatatggcgc aaccagagtt cacgacggcc atctgggatt atttgtctga acgtctgact 300

ccgaagaata tccagcaagg gcaggagctt ctgcaaaaag agccagttct gaacgaggta 360

gagcgtcact acggtgtgga tgcgaagatt atcgcggcca tctggtgtat tgaaagcggc 420

tacggtaagg atattggtag tcgcgatgtg attcgttcct tggccacgct tgcttacaag 480

ggccggcgga tggattacgg ggctacacag ttgatggccg cccttcatat cgtgcaaaac 540

-continued

```
aaagacatcg cccgtgcgca attgattggc tcgtgggctg gcgcgatggg gcagacgcaa    600

ttcatcccga cgacctatct cgactatgca gttgatttta accacgacaa tcggcgcgac    660

gtttggagtt cccgggccga tgcgctggcc tccactgcct cttatttaca acgcagcgct    720

tggaactcgc gcgtctcttg gggacaggag gtgcagttgc ccgagaattt cgattacgct    780

caggctgaca tgtcgatcaa gaagcccgtt gccgaatggc aacggctcgg ggtgatggga    840

acgaagcaag cgattccggg cgagctcgca caggagcaag catcggtcct gctgcccgca    900

ggttatcgcg ggccagcatt tatggtccta agtaatttcc gtagcatcct gcgctataac    960

aactccactg cctatgcgct aacgatcggg ctactagccg acagttatgc tggcgggacc   1020

ggcgtgtctc acccgtggcc aactgataat cctcccttgg gcagcattgc gcaggtaacc   1080

gatttgcaga aactgctgac tgctaagggc tactccctgg gtgctgctga cggtgttata   1140

ggggcgatga cccgggcggc catccgggct taccagaagg atcagcattt gccacccgac   1200

ggttacgcca gcactgtact actggagagc ctgcgccgat ag                      1242
```

<210> SEQ ID NO 40
<211> LENGTH: 413
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 40

```
Met Arg Ser Arg Val Ile Thr Thr Ser Leu Val Val Ile Met Leu Ser
  1               5                  10                  15

Cys Ala Ser Ala Ala Pro Ala Cys Phe Ser Ala Asp Met Thr Pro Ser
             20                  25                  30

Val Ser Asn Glu Ser Thr Ser Glu Ala Asp Phe Gln Gln Trp Leu Ala
         35                  40                  45

Thr Phe Arg Ser Asn Ala Thr Thr Lys Gly Ile Asp Thr Ala Thr Leu
     50                  55                  60

Asp Leu Ala Phe Gln Asn Ile Thr Leu Asp Pro Thr Val His Gln Leu
 65                  70                  75                  80

Asp Met Ala Gln Pro Glu Phe Thr Thr Ala Ile Trp Asp Tyr Leu Ser
                 85                  90                  95

Glu Arg Leu Thr Pro Lys Asn Ile Gln Gln Gly Gln Glu Leu Leu Gln
            100                 105                 110

Lys Glu Pro Val Leu Asn Glu Val Glu Arg His Tyr Gly Val Asp Ala
        115                 120                 125

Lys Ile Ile Ala Ala Ile Trp Cys Ile Glu Ser Gly Tyr Gly Lys Asp
    130                 135                 140

Ile Gly Ser Arg Asp Val Ile Arg Ser Leu Ala Thr Leu Ala Tyr Lys
145                 150                 155                 160

Gly Arg Arg Met Asp Tyr Gly Ala Thr Gln Leu Met Ala Ala Leu His
                165                 170                 175

Ile Val Gln Asn Lys Asp Ile Ala Arg Ala Gln Leu Ile Gly Ser Trp
            180                 185                 190

Ala Gly Ala Met Gly Gln Thr Gln Phe Ile Pro Thr Thr Tyr Leu Asp
        195                 200                 205

Tyr Ala Val Asp Phe Asn His Asp Asn Arg Arg Asp Val Trp Ser Ser
    210                 215                 220

Arg Ala Asp Ala Leu Ala Ser Thr Ala Ser Tyr Leu Gln Arg Ser Ala
225                 230                 235                 240

Trp Asn Ser Arg Val Ser Trp Gly Gln Glu Val Gln Leu Pro Glu Asn
                245                 250                 255
```

-continued

```
Phe Asp Tyr Ala Gln Ala Asp Met Ser Ile Lys Lys Pro Val Ala Glu
            260                 265                 270

Trp Gln Arg Leu Gly Val Met Gly Thr Lys Gln Ala Ile Pro Gly Glu
        275                 280                 285

Leu Ala Gln Glu Gln Ala Ser Val Leu Leu Pro Ala Gly Tyr Arg Gly
    290                 295                 300

Pro Ala Phe Met Val Leu Ser Asn Phe Arg Ser Ile Leu Arg Tyr Asn
305                 310                 315                 320

Asn Ser Thr Ala Tyr Ala Leu Thr Ile Gly Leu Leu Ala Asp Ser Tyr
                325                 330                 335

Ala Gly Gly Thr Gly Val Ser His Pro Trp Pro Thr Asp Asn Pro Pro
            340                 345                 350

Leu Gly Ser Ile Ala Gln Val Thr Asp Leu Gln Lys Leu Leu Thr Ala
        355                 360                 365

Lys Gly Tyr Ser Leu Gly Ala Ala Asp Gly Val Ile Gly Ala Met Thr
    370                 375                 380

Arg Ala Ala Ile Arg Ala Tyr Gln Lys Asp Gln His Leu Pro Pro Asp
385                 390                 395                 400

Gly Tyr Ala Ser Thr Val Leu Leu Glu Ser Leu Arg Arg
                405                 410
```

<210> SEQ ID NO 41
<211> LENGTH: 960
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 41

```
atgcttgctc ctgacggcgt agaaatcgat atcgtgctat caggtatatg cggaactgat     60

ctggcggtat tgtcgggccg tgaaggtgga gaggtgggca ttatacgcgg gcacgaagca    120

gttggcatta ttatcgatgt aggtaaggat gtagtacacc tacaaaaagg gatgcgggtg    180

gtggttgatc ccaacgaata ctgtggcgtt tgcgaacctt gccgtcttgc taaaacgcac    240

ctatgcaatg ggggggtgaa cgctgggttg gatatcgcag gtgtcaacaa acatggaact    300

tttgccgagc gcttcgttac tcgtgagcgt tttgtgtatc aattgccaga cgatatgagc    360

tgggcagctg gtgtgttggt tgagcctgtt gcctgcattc tgaataatat agaccaggcg    420

ttcattcgag cgggagagcg tgtgttgatc ctagggtctg gccctatgag tctgattgcg    480

cagatcgttc tgcgctcaat gggagttgac acgctcgcca ctgatcgaaa cacacatcgc    540

atacagttcg gccgctcaca aagtcttgat gttatacatg ccgatgatct tgagttgcag    600

atgcagcacc aagaaaagtt tgatgttgtt atcgatactg tcggtaatca gatcgataca    660

gcttcacgct acatcggtcg cggtgggaga attgtacttt ttggatttga tagtgactat    720

cactacatgc tgcctgtaaa gtacttcctg gttaacgcta tcagtattat ttctgctgga    780

gaatacaatc agcactttcc tagagcaatt cgtcttgtgc aaaaacttcc tgagctaggg    840

cggctggtaa cgcatcgcta cgtactagaa aatcactcgg aggttttcga tgcacttctg    900

aacgatgctt ccgcccccaa tataaaaagc gtattcacac caaatctcgc ttatctttaa    960
```

<210> SEQ ID NO 42
<211> LENGTH: 319
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 42

```
Met Leu Ala Pro Asp Gly Val Glu Ile Asp Ile Val Leu Ser Gly Ile
  1               5                  10                  15

Cys Gly Thr Asp Leu Ala Val Leu Ser Gly Arg Glu Gly Gly Glu Val
             20                  25                  30

Gly Ile Ile Arg Gly His Glu Ala Val Gly Ile Ile Ile Asp Val Gly
         35                  40                  45

Lys Asp Val Val His Leu Gln Lys Gly Met Arg Val Val Val Asp Pro
     50                  55                  60

Asn Glu Tyr Cys Gly Val Cys Glu Pro Cys Arg Leu Ala Lys Thr His
 65                  70                  75                  80

Leu Cys Asn Gly Gly Val Asn Ala Gly Leu Asp Ile Ala Gly Val Asn
                 85                  90                  95

Lys His Gly Thr Phe Ala Glu Arg Phe Val Thr Arg Glu Arg Phe Val
            100                 105                 110

Tyr Gln Leu Pro Asp Asp Met Ser Trp Ala Ala Gly Val Leu Val Glu
        115                 120                 125

Pro Val Ala Cys Ile Leu Asn Asn Ile Asp Gln Ala Phe Ile Arg Ala
    130                 135                 140

Gly Glu Arg Val Leu Ile Leu Gly Ser Gly Pro Met Ser Leu Ile Ala
145                 150                 155                 160

Gln Ile Val Leu Arg Ser Met Gly Val Asp Thr Leu Ala Thr Asp Arg
                165                 170                 175

Asn Thr His Arg Ile Gln Phe Gly Arg Ser Gln Ser Leu Asp Val Ile
            180                 185                 190

His Ala Asp Asp Leu Glu Leu Gln Met Gln His Gln Glu Lys Phe Asp
        195                 200                 205

Val Val Ile Asp Thr Val Gly Asn Gln Ile Asp Thr Ala Ser Arg Tyr
    210                 215                 220

Ile Gly Arg Gly Gly Arg Ile Val Leu Phe Gly Phe Asp Ser Asp Tyr
225                 230                 235                 240

His Tyr Met Leu Pro Val Lys Tyr Phe Leu Val Asn Ala Ile Ser Ile
                245                 250                 255

Ile Ser Ala Gly Glu Tyr Asn Gln His Phe Pro Arg Ala Ile Arg Leu
            260                 265                 270

Val Gln Lys Leu Pro Glu Leu Gly Arg Leu Val Thr His Arg Tyr Val
        275                 280                 285

Leu Glu Asn His Ser Glu Val Phe Asp Ala Leu Leu Asn Asp Ala Ser
    290                 295                 300

Ala Pro Asn Ile Lys Ser Val Phe Thr Pro Asn Leu Ala Tyr Leu
305                 310                 315
```

<210> SEQ ID NO 43
<211> LENGTH: 675
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 43

```
atgaaagtta ctgtattcag tcagatatca attgatggca agttgacgat gggcaaaggc     60

gcatccagca agccgttgtt tcagaacttt gatgatgatg acatgcgttt tattcataag    120

ttccgcggcg aagtcgacgc aatcatggta gggcgcaata caattgttac tgacgatcca    180

caattgacca atcgctatga gtcgggtcgt aacccaatac gtatcattcc caccacctcc    240

ttagatctgc ctacttccgc cagtattttc aaatcaccag agaaaactat tatcgcaact    300
```

-continued

```
agcgaacagg ctcgtgatca tgaaatggtc aaacatatcc gtgcttgtgg aaaggaggtg    360

ctctttgccg gtgcaaagca tgtcgacttt acacgacttt tccctatgct ggaggcgcgc    420

ggaataaacc acatcatggt tgagggcggt ggccacctga actggcaggt attcaatctc    480

gatctggtag atgaaattat actcatgcag gtgcctatca tcataggtgg tgcggcaact    540

gcaacgcttg ctgacggggt ggggtatcgg gatatcaaca tggccaattc gtttacgctg    600

catgctttag aagcacgccc ccattacaat ctcatgcact tcaagcgcga atcgaacaat    660

cggagcccgt actga                                                     675


<210> SEQ ID NO 44
<211> LENGTH: 224
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 44

Met Lys Val Thr Val Phe Ser Gln Ile Ser Ile Asp Gly Lys Leu Thr
  1               5                  10                  15

Met Gly Lys Gly Ala Ser Ser Lys Pro Leu Phe Gln Asn Phe Asp Asp
             20                  25                  30

Asp Asp Met Arg Phe Ile His Lys Phe Arg Gly Glu Val Asp Ala Ile
         35                  40                  45

Met Val Gly Arg Asn Thr Ile Val Thr Asp Asp Pro Gln Leu Thr Asn
     50                  55                  60

Arg Tyr Glu Ser Gly Arg Asn Pro Ile Arg Ile Ile Pro Thr Thr Ser
 65                  70                  75                  80

Leu Asp Leu Pro Thr Ser Ala Ser Ile Phe Lys Ser Pro Glu Lys Thr
                 85                  90                  95

Ile Ile Ala Thr Ser Glu Gln Ala Arg Asp His Glu Met Val Lys His
            100                 105                 110

Ile Arg Ala Cys Gly Lys Glu Val Leu Phe Ala Gly Ala Lys His Val
        115                 120                 125

Asp Phe Thr Arg Leu Phe Pro Met Leu Glu Ala Arg Gly Ile Asn His
    130                 135                 140

Ile Met Val Glu Gly Gly Gly His Leu Asn Trp Gln Val Phe Asn Leu
145                 150                 155                 160

Asp Leu Val Asp Glu Ile Ile Leu Met Gln Val Pro Ile Ile Ile Gly
                165                 170                 175

Gly Ala Ala Thr Ala Thr Leu Ala Asp Gly Val Gly Tyr Arg Asp Ile
            180                 185                 190

Asn Met Ala Asn Ser Phe Thr Leu His Ala Leu Glu Ala Arg Pro His
        195                 200                 205

Tyr Asn Leu Met His Phe Lys Arg Glu Ser Asn Asn Arg Ser Pro Tyr
    210                 215                 220


<210> SEQ ID NO 45
<211> LENGTH: 588
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 45

atggagcagg aaaagagttc ctgtttgcgc tacggcgtga cccttaatga aaaagatctg     60

tcacgttttt tgggaactac acagcactac atgtggagca cgattaaaaa tgagtacgcg    120

ctcactgaat ccatcgacca cttgatggca cagcatcaac agcaattaat gcgctcaatc    180

agttttgaat tgtttcaatc catgcctggc gtggaggcgc ttctcaattt actggagcat    240
```

-continued

```
accggagtgc cctgtgccgt agcctcttcg tctccacgta atttggtcga gcttatattg    300

aagaaaacga aattgcgtcg atttttcaaa gaggttattt gtggtactga tgttaaagag    360

agtaaaccga atccggagat ttttcttacg gcggccaagg gacttggagt gtcacctcgt    420

gcatgtctgg ttattgaaga ctcccatcac ggtgttaccg ctgcgaaggc cgcccatatg    480

ttttgtatag gtttgcgtca ttccagctca tttcagcagg atctgagcgc tgctgatctg    540

atcgccaata atcattatga catcaagcaa tggtttgcag aaaaatag                 588


<210> SEQ ID NO 46
<211> LENGTH: 195
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 46

Met Glu Gln Glu Lys Ser Ser Cys Leu Arg Tyr Gly Val Thr Leu Asn
  1               5                  10                  15

Glu Lys Asp Leu Ser Arg Phe Leu Gly Thr Thr Gln His Tyr Met Trp
             20                  25                  30

Ser Thr Ile Lys Asn Glu Tyr Ala Leu Thr Glu Ser Ile Asp His Leu
         35                  40                  45

Met Ala Gln His Gln Gln Gln Leu Met Arg Ser Ile Ser Phe Glu Leu
     50                  55                  60

Phe Gln Ser Met Pro Gly Val Glu Ala Leu Leu Asn Leu Leu Glu His
 65                  70                  75                  80

Thr Gly Val Pro Cys Ala Val Ala Ser Ser Ser Pro Arg Asn Leu Val
                 85                  90                  95

Glu Leu Ile Leu Lys Lys Thr Lys Leu Arg Arg Phe Phe Lys Glu Val
            100                 105                 110

Ile Cys Gly Thr Asp Val Lys Glu Ser Lys Pro Asn Pro Glu Ile Phe
        115                 120                 125

Leu Thr Ala Ala Lys Gly Leu Gly Val Ser Pro Arg Ala Cys Leu Val
    130                 135                 140

Ile Glu Asp Ser His His Gly Val Thr Ala Ala Lys Ala Ala His Met
145                 150                 155                 160

Phe Cys Ile Gly Leu Arg His Ser Ser Ser Phe Gln Gln Asp Leu Ser
                165                 170                 175

Ala Ala Asp Leu Ile Ala Asn Asn His Tyr Asp Ile Lys Gln Trp Phe
            180                 185                 190

Ala Glu Lys
        195


<210> SEQ ID NO 47
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 47

atgaatgcgt tcgcaaccgg tcagcttgaa tacagcctga aaaagctggg atacgatgcc     60

gccgctttgc aggccctgcg cgaagaaggg tacttgctgt ggaaagggaa aaacgaccag    120

accagcttgc tggtgccctc ggccgatctg gatgcacttt tcgttatcaa cacgttgagc    180

tacatcgacc ccgagcatga cggacgtctg ctggcgcttg cattgcacct taacctgtcc    240

cctgtccata cgatgagcgc ctgcatagcc ctcgatgtcg agcaaaacac gttatgcctg    300

cgctacaccc atgaccttgg cgggagcggg gctgataccc tgttgcttgc gctcgaaaac    360
```

-continued

```
gcccaggcgc tggccgaaca ggtcaggcag gtgatcgaaa ccttcaggcg tgaccaaggg    420

cgtccgtccg ggcaaacgtc tttgtcccgg caatccagtg ctctgatgcg ataa         474


<210> SEQ ID NO 48
<211> LENGTH: 157
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 48

Met Asn Ala Phe Ala Thr Gly Gln Leu Glu Tyr Ser Leu Lys Lys Leu
  1               5                  10                  15

Gly Tyr Asp Ala Ala Ala Leu Gln Ala Leu Arg Glu Glu Gly Tyr Leu
             20                  25                  30

Leu Trp Lys Gly Lys Asn Asp Gln Thr Ser Leu Leu Val Pro Ser Ala
         35                  40                  45

Asp Leu Asp Ala Leu Phe Val Ile Asn Thr Leu Ser Tyr Ile Asp Pro
     50                  55                  60

Glu His Asp Gly Arg Leu Leu Ala Leu Ala Leu His Leu Asn Leu Ser
 65                  70                  75                  80

Pro Val His Thr Met Ser Ala Cys Ile Ala Leu Asp Val Glu Gln Asn
                 85                  90                  95

Thr Leu Cys Leu Arg Tyr Thr His Asp Leu Gly Gly Ser Gly Ala Asp
            100                 105                 110

Thr Leu Leu Leu Ala Leu Glu Asn Ala Gln Ala Leu Ala Glu Gln Val
        115                 120                 125

Arg Gln Val Ile Glu Thr Phe Arg Arg Asp Gln Gly Arg Pro Ser Gly
    130                 135                 140

Gln Thr Ser Leu Ser Arg Gln Ser Ser Ala Leu Met Arg
145                 150                 155


<210> SEQ ID NO 49
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 49

atgaaaatat ccggctccac atcgcctgca cacacttcaa cgaattccgc gcagaagtcc     60

tcttcaaaag ggctgctgag tggtttggcc aagcatttca aggggatgct cgtttctggc    120

aacacttctg gtcattcggc gctcgggcat tacgcgtcat ccagcagcgg ctccaaaggc    180

aaggcaccgg tacgggacga ttacagcaac ggaccgcaaa cacgccttaa caacacacct    240

ctgaaacgag cactggcccg agagcttgat cgctttggct acggttcatc ggcgaccgag    300

tcttttgacc gctcattgca gcgtaaggat aaaaatccag agcttgggaa ggtctga       357


<210> SEQ ID NO 50
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 50

Met Lys Ile Ser Gly Ser Thr Ser Pro Ala His Thr Ser Thr Asn Ser
  1               5                  10                  15

Ala Gln Lys Ser Ser Ser Lys Gly Leu Leu Ser Gly Leu Ala Lys His
             20                  25                  30

Phe Lys Gly Met Leu Val Ser Gly Asn Thr Ser Gly His Ser Ala Leu
         35                  40                  45
```

-continued

```
Gly His Tyr Ala Ser Ser Ser Ser Gly Ser Lys Gly Lys Ala Pro Val
     50                  55                  60

Arg Asp Asp Tyr Ser Asn Gly Pro Gln Thr Arg Leu Asn Asn Thr Pro
 65                  70                  75                  80

Leu Lys Arg Ala Leu Ala Arg Glu Leu Asp Arg Phe Gly Tyr Gly Ser
                85                  90                  95

Ser Ala Thr Glu Ser Phe Asp Arg Ser Leu Gln Arg Lys Asp Lys Asn
            100                 105                 110

Pro Glu Leu Gly Lys Val
        115
```

<210> SEQ ID NO 51
<211> LENGTH: 1299
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 51

```
atgaaaaaat gtattgctct gctccttact ctggtcgtct gcgaaggtgc attggcagga     60

acggcacgtg atgaacagaa catcacgtct tacatcgaca gtcacggcac cgaacagatc    120

gcgttgcttg agaagctggt caacatcaac agcgggacag acaacgttga gggtgtcgtc    180

aaggtcggta acctgatcaa gccggagctg gaggcgttgg gtttcgagac cgcctggcac    240

gacctgccct cggcaatgaa ccatgccggc agccttgtcg ctgtgcatga cggcagcaag    300

tctgcaaaac gtattctgct gataggccat ctggatacgg tctttcctca aacaagccgc    360

tttcagacgt tcgcttacct ggacggcggc aaaaaagcca agggccccgg cgtcattgat    420

gacaaaggcg gcgtggtcac gatgctttat gcattgcagg cgctcaagca cagcggcgcg    480

ctggaaaaga tgaacatctc ggtagtcttg ataggcgatg aagagctggc ggccaaaccg    540

accgagattt ccagagagtg gctgatcgcc gaagccaaaa gaagcgacat tgcgctgggc    600

ttcgaattcg ccttgtcgcc caatcaactg atcaccgagc gaagagggct gagcgaatgg    660

tttttgacca gcaccggcat cgacaaacat tcagcgacga tctttcagcc tgagaccggt    720

tttggtgcga tgtacgagtc ggcccgagtg cttgacgaga ttcgtcagaa actgtcgaac    780

gagcagggcc tgaccatcaa tccgggactc attctgggcg gctcaacggc tgtggaagat    840

agcgccagtg ggcaaggcac ggcttctgga agaaagacaa cagttgcccg gatcacgtcg    900

gtgcatggtg atttgcgctt cagcagtgaa gaccagaggg cctctgcgga aacccgaatg    960

aaggacatag ccagtcaccc gctgccgcag accaacagcg acctgaaaat aaaagccatc   1020

atgccggtca tggcggatcg cgaaagcaat cgccaactac tggcagccta cagtcaggtc   1080

agccaggatc tcgacggacc tgctttggag tcggcgcctt cagcagaacg aggcggcgca   1140

gatatttcct atgtgaacaa gtatgtgact gcgagcctgg acggtcttgg tgcgtggggg   1200

gcaggtgcgc acagtgaaaa tgaaaccatc gagttgggct ccttgcccgt ggtgacgaaa   1260

cgggcggcta ttttcctgag ccgctatggt aaccagtga                          1299
```

<210> SEQ ID NO 52
<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 52

```
Met Lys Lys Cys Ile Ala Leu Leu Leu Thr Leu Val Val Cys Glu Gly
  1               5                  10                  15
```

-continued

```
Ala Leu Ala Gly Thr Ala Arg Asp Glu Gln Asn Ile Thr Ser Tyr Ile
            20                  25                  30

Asp Ser His Gly Thr Glu Gln Ile Ala Leu Leu Glu Lys Leu Val Asn
        35                  40                  45

Ile Asn Ser Gly Thr Asp Asn Val Glu Gly Val Val Lys Val Gly Asn
    50                  55                  60

Leu Ile Lys Pro Glu Leu Glu Ala Leu Gly Phe Glu Thr Ala Trp His
65                  70                  75                  80

Asp Leu Pro Ser Ala Met Asn His Ala Gly Ser Leu Val Ala Val His
                85                  90                  95

Asp Gly Ser Lys Ser Ala Lys Arg Ile Leu Leu Ile Gly His Leu Asp
            100                 105                 110

Thr Val Phe Pro Gln Thr Ser Arg Phe Gln Thr Phe Ala Tyr Leu Asp
        115                 120                 125

Gly Gly Lys Lys Ala Lys Gly Pro Gly Val Ile Asp Asp Lys Gly Gly
    130                 135                 140

Val Val Thr Met Leu Tyr Ala Leu Gln Ala Leu Lys His Ser Gly Ala
145                 150                 155                 160

Leu Glu Lys Met Asn Ile Ser Val Val Leu Ile Gly Asp Glu Glu Leu
                165                 170                 175

Ala Ala Lys Pro Thr Glu Ile Ser Arg Glu Trp Leu Ile Ala Glu Ala
            180                 185                 190

Lys Arg Ser Asp Ile Ala Leu Gly Phe Glu Phe Ala Leu Ser Pro Asn
        195                 200                 205

Gln Leu Ile Thr Glu Arg Arg Gly Leu Ser Glu Trp Phe Leu Thr Ser
    210                 215                 220

Thr Gly Ile Asp Lys His Ser Ala Thr Ile Phe Gln Pro Glu Thr Gly
225                 230                 235                 240

Phe Gly Ala Met Tyr Glu Ser Ala Arg Val Leu Asp Glu Ile Arg Gln
                245                 250                 255

Lys Leu Ser Asn Glu Gln Gly Leu Thr Ile Asn Pro Gly Leu Ile Leu
            260                 265                 270

Gly Gly Ser Thr Ala Val Glu Asp Ser Ala Ser Gly Gln Gly Thr Ala
        275                 280                 285

Ser Gly Arg Lys Thr Thr Val Ala Arg Ile Thr Ser Val His Gly Asp
    290                 295                 300

Leu Arg Phe Ser Ser Glu Asp Gln Arg Ala Ser Ala Glu Thr Arg Met
305                 310                 315                 320

Lys Asp Ile Ala Ser His Pro Leu Pro Gln Thr Asn Ser Asp Leu Lys
                325                 330                 335

Ile Lys Ala Ile Met Pro Val Met Ala Asp Arg Glu Ser Asn Arg Gln
            340                 345                 350

Leu Leu Ala Ala Tyr Ser Gln Val Ser Gln Asp Leu Asp Gly Pro Ala
        355                 360                 365

Leu Glu Ser Ala Pro Ser Ala Glu Arg Gly Gly Ala Asp Ile Ser Tyr
    370                 375                 380

Val Asn Lys Tyr Val Thr Ala Ser Leu Asp Gly Leu Gly Ala Trp Gly
385                 390                 395                 400

Ala Gly Ala His Ser Glu Asn Glu Thr Ile Glu Leu Gly Ser Leu Pro
                405                 410                 415

Val Val Thr Lys Arg Ala Ala Ile Phe Leu Ser Arg Tyr Gly Asn Gln
            420                 425                 430
```

-continued

<210> SEQ ID NO 53
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 53

atgaacccta taacacacag ctttagtcat cttgggtttt caaacgctca aagtacgtca 60

gcgctggcgc ccggcggtaa taaagtgccg aactttgttt cgcgagggcg aggcaaagga 120

gtcccgcttg agcatttcaa caccgctgat gagtatcgtt tggcacgcca gcagggcggc 180

gtgctgaaat caatagacgg cagagagttc atgctactgc tgcagaagta cacggccgcc 240

gaaacaagcg acgaagaatt tgcggatttg agggccgcca taccgcgcta ttccattgac 300

ctggccgagc cgggtcaaac taaagtgctt tatcgggga tatcgctgcc ggagaagact 360

gcggcgcgat tactgaatat ctcttggggt tacgaaagtc gcgaaatagc ccatggtctt 420

atccatggct tgcgggtagt taaggaaggt ctgaagtag 459

<210> SEQ ID NO 54
<211> LENGTH: 152
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 54

Met Asn Pro Ile Thr His Ser Phe Ser His Leu Gly Phe Ser Asn Ala
1 5 10 15

Gln Ser Thr Ser Ala Leu Ala Pro Gly Gly Asn Lys Val Pro Asn Phe
20 25 30

Val Ser Arg Gly Arg Gly Lys Gly Val Pro Leu Glu His Phe Asn Thr
35 40 45

Ala Asp Glu Tyr Arg Leu Ala Arg Gln Gln Gly Gly Val Leu Lys Ser
50 55 60

Ile Asp Gly Arg Glu Phe Met Leu Leu Leu Gln Lys Tyr Thr Ala Ala
65 70 75 80

Glu Thr Ser Asp Glu Glu Phe Ala Asp Leu Arg Ala Ala Ile Pro Arg
85 90 95

Tyr Ser Ile Asp Leu Ala Glu Pro Gly Gln Thr Lys Val Leu Tyr Arg
100 105 110

Gly Ile Ser Leu Pro Glu Lys Thr Ala Ala Arg Leu Leu Asn Ile Ser
115 120 125

Trp Gly Tyr Glu Ser Arg Glu Ile Ala His Gly Leu Ile His Gly Leu
130 135 140

Arg Val Val Lys Glu Gly Leu Lys
145 150

<210> SEQ ID NO 55
<211> LENGTH: 2700
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 55

atgactactc tgaccaccag acagatacaa ctcgcccacg cttggacatc cgttcataca 60

ggcgctggcc tggccctgga ctgggtcgcc gatgtggccg aaaaggtcga ggaaatcgcc 120

accaaggccg acgccctcag ccgtgacttg caccgcgcgc gcaacctgtc ccgcagcctt 180

gggcgggtct cgacgacacc catgggtatc ggtttcttcg gcttgtctca ggcaggcaag 240

agctacctga tttccgctct ggcggcggac gagaaaggcc agttgctgac ccggctgggt 300

-continued

```
actcagcaac tggacttcat caagcacgtg aacccggtgg gcggcggtaa ggaggccacc    360

ggtctggtca cgcggttcac ccgcaccgcc gcgccaagtc tggacccgca ctttccggtg    420

gagctgcgtc tgtttcgcga ggtcgagatc gccatcattt tggccaacgc ctggtttgag    480

gatttcgatc atcagcgctt gaacagccaa gtcaccgatg cgcagatcga tgccctttg    540

cagcgtttcg aggggcaatt ggcagccgct ccgacacctg gcgtcagcag tgacgacgtg    600

gtgctgctat gggattacct ggagcaccat tacgctaacg ccatgcgccc gctgaacgcc    660

cgttattggc cttgcgtggt caaactggcg ccgcgcttgt cggcacgcga gcgcgctcaa    720

ttgttcgagc cgctgtgggg cggcatcggc aaaatgaccg aaacctatga gcaactggcc    780

tcggccctgc accgcctggg gctggcagag acagtttttg cgcccatcag cgcgctggtc    840

accgagcgcg atgggcaact ggtacaaagc aaaagcatca tcaacgtcga cattctcagc    900

cgtcttggcg gcagcgcgga ctcggccatc gaggtacgtc cggccagtga aggcactttg    960

cgccctgccg tgtcggtgaa tcgggccgaa ctggcggcgc tcaccaacga gttgattttt   1020

cgcctggata acgaaccggc caacgccatc gtcaatagcg tcgatctgct cgacttcccg   1080

ggctaccgca gccggcagaa gctgatgagc atcaacgagg ccagcgaagt cgacagcaat   1140

ggcaccgcca acaatccggt cgccaggctg ttgctgcgcg gcaaggtcgc ttacttgttt   1200

gagcgttaca ccaacgagca ggaaatgaac gcgctggtga tgtgcaccag caccttcaag   1260

cagagcgaag tggtgagcgt cggtccggta ctcaagagct ggatcgacaa gacccaaggc   1320

accagccccc agcagcgcga tggtcgggcc agcggtctga tctgggcgtt gaccatgtgt   1380

gacggcttta tcggcggcgc gctcaacggc gaggttgtgc agtttcccga aggttgcgac   1440

aacatgctca aactgaccat gatcgagcga ttcggcaacg aagactggat gaaacaatgg   1500

ggcagcacgc ctttcaaaaa cacctatctg gtgcgcaagc cgcgcttcaa gaccagcttc   1560

atcgagttgg cggcggacgg tgaagaacgc gcttacaacg actcatcgca ctctgcgtta   1620

caggcattgc aacaagcgtt cagcaacagt gaactggtca agcgccatgt ggcagaaccg   1680

caggacgcct ggcaggcaat gctgacactg aacgacggcg gcatgactcg tttcagctcg   1740

gcgttcagcc cgattgccaa catcgacttc aagttacagc gtattgccga gcaactggac   1800

gagttgatgg tgcaattact gccgcgcctg gagcagtact acgaagccgg tggcgaagac   1860

gaacgggcca ggaagaaggt tatcgccaac ctgattgccc gcccgttcgc gaccacgccg   1920

cacggcaaac acgtgcttgg cgaactgctc ggttacatgt cgttgccgga acagcagttg   1980

cgcgaccttt acctgaacgg tgatttcgcc agccctgcca gcgacgccac tgcaccggtg   2040

caggccgtcg gcaagcctga agtggaatac gacatattcg gcgaggccat cgcagccact   2100

gccacggtgg aaatacccgc ggcaccggcc gtagcgccgc aataccagag ccacgaacac   2160

cgtttcgccc gagcggcctt cgacctgtgg gcaacgcacc tgcgcaacct cagccgtcgc   2220

cagcacctgc tggacctgtt ggagctgcct gccgaggcca tcgccctgct ggtcaaggaa   2280

ctggtggtct gcgccgagcg cctggacttg ccattgcagc tcagcaacgc gctgctcaag   2340

cgcgcccaga gcggtgtgcg caaagaaaac ctggtgcagc gccaagtgct gaccgcgcaa   2400

ctgctgctca acgacttcgc cgcctggttc gggcacaccg cccagccggc gggtcagcgg   2460

ccaacgggcc tgctgggtgc caaacaaccg ctgtttgctt tttatcaaaa ggaaatgcca   2520

gggcgcttcc cgcacctcgc agcgcaagcc gacgaccaga gcgtgatttt cgccgatgac   2580

tggatttctg gcattgccat tcatacccag aaaaacgtcg gccaccgcaa gggcaaagaa   2640

atcactcctg agcagaacga ggccatgggc cgcgtcatcc aggcgttcaa agcgagataa   2700
```

-continued

<210> SEQ ID NO 56
<211> LENGTH: 899
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 56

Met Thr Thr Leu Thr Thr Arg Gln Ile Gln Leu Ala His Ala Trp Thr
1 5 10 15

Ser Val His Thr Gly Ala Gly Leu Ala Leu Asp Trp Val Ala Asp Val
20 25 30

Ala Glu Lys Val Glu Glu Ile Ala Thr Lys Ala Asp Ala Leu Ser Arg
35 40 45

Asp Leu His Arg Ala Arg Asn Leu Ser Arg Ser Leu Gly Arg Val Ser
50 55 60

Thr Thr Pro Met Gly Ile Gly Phe Phe Gly Leu Ser Gln Ala Gly Lys
65 70 75 80

Ser Tyr Leu Ile Ser Ala Leu Ala Ala Asp Glu Lys Gly Gln Leu Leu
85 90 95

Thr Arg Leu Gly Thr Gln Gln Leu Asp Phe Ile Lys His Val Asn Pro
100 105 110

Val Gly Gly Gly Lys Glu Ala Thr Gly Leu Val Thr Arg Phe Thr Arg
115 120 125

Thr Ala Ala Pro Ser Leu Asp Pro His Phe Pro Val Glu Leu Arg Leu
130 135 140

Phe Arg Glu Val Glu Ile Ala Ile Ile Leu Ala Asn Ala Trp Phe Glu
145 150 155 160

Asp Phe Asp His Gln Arg Leu Asn Ser Gln Val Thr Asp Ala Gln Ile
165 170 175

Asp Ala Leu Leu Gln Arg Phe Glu Gly Gln Leu Ala Ala Ala Pro Thr
180 185 190

Pro Gly Val Ser Ser Asp Asp Val Val Leu Leu Trp Asp Tyr Leu Glu
195 200 205

His His Tyr Ala Asn Ala Met Arg Pro Leu Asn Ala Arg Tyr Trp Pro
210 215 220

Cys Val Val Lys Leu Ala Pro Arg Leu Ser Ala Arg Glu Arg Ala Gln
225 230 235 240

Leu Phe Glu Pro Leu Trp Gly Gly Ile Gly Lys Met Thr Glu Thr Tyr
245 250 255

Glu Gln Leu Ala Ser Ala Leu His Arg Leu Gly Leu Ala Glu Thr Val
260 265 270

Phe Ala Pro Ile Ser Ala Leu Val Thr Glu Arg Asp Gly Gln Leu Val
275 280 285

Gln Ser Lys Ser Ile Ile Asn Val Asp Ile Leu Ser Arg Leu Gly Gly
290 295 300

Ser Ala Asp Ser Ala Ile Glu Val Arg Pro Ala Ser Glu Gly Thr Leu
305 310 315 320

Arg Pro Ala Val Ser Val Asn Arg Ala Glu Leu Ala Ala Leu Thr Asn
325 330 335

Glu Leu Ile Phe Arg Leu Asp Asn Glu Pro Ala Asn Ala Ile Val Asn
340 345 350

Ser Val Asp Leu Leu Asp Phe Pro Gly Tyr Arg Ser Arg Gln Lys Leu
355 360 365

Met Ser Ile Asn Glu Ala Ser Glu Val Asp Ser Asn Gly Thr Ala Asn
370 375 380

-continued

```
Asn Pro Val Ala Arg Leu Leu Leu Arg Gly Lys Val Ala Tyr Leu Phe
385                 390                 395                 400

Glu Arg Tyr Thr Asn Glu Gln Glu Met Asn Ala Leu Val Met Cys Thr
                405                 410                 415

Ser Thr Phe Lys Gln Ser Glu Val Val Ser Val Gly Pro Val Leu Lys
            420                 425                 430

Ser Trp Ile Asp Lys Thr Gln Gly Thr Ser Pro Gln Gln Arg Asp Gly
        435                 440                 445

Arg Ala Ser Gly Leu Ile Trp Ala Leu Thr Met Cys Asp Gly Phe Ile
    450                 455                 460

Gly Gly Ala Leu Asn Gly Glu Val Val Gln Phe Pro Glu Gly Cys Asp
465                 470                 475                 480

Asn Met Leu Lys Leu Thr Met Ile Glu Arg Phe Gly Asn Glu Asp Trp
                485                 490                 495

Met Lys Gln Trp Gly Ser Thr Pro Phe Lys Asn Thr Tyr Leu Val Arg
            500                 505                 510

Lys Pro Arg Phe Lys Thr Ser Phe Ile Glu Leu Ala Ala Asp Gly Glu
        515                 520                 525

Glu Arg Ala Tyr Asn Asp Ser Ser His Ser Ala Leu Gln Ala Leu Gln
    530                 535                 540

Gln Ala Phe Ser Asn Ser Glu Leu Val Lys Arg His Val Ala Glu Pro
545                 550                 555                 560

Gln Asp Ala Trp Gln Ala Met Leu Thr Leu Asn Asp Gly Gly Met Thr
                565                 570                 575

Arg Phe Ser Ser Ala Phe Ser Pro Ile Ala Asn Ile Asp Phe Lys Leu
            580                 585                 590

Gln Arg Ile Ala Glu Gln Leu Asp Glu Leu Met Val Gln Leu Leu Pro
        595                 600                 605

Arg Leu Glu Gln Tyr Tyr Glu Ala Gly Gly Glu Asp Glu Arg Ala Arg
    610                 615                 620

Lys Lys Val Ile Ala Asn Leu Ile Ala Arg Pro Phe Ala Thr Thr Pro
625                 630                 635                 640

His Gly Lys His Val Leu Gly Glu Leu Leu Gly Tyr Met Ser Leu Pro
                645                 650                 655

Glu Gln Gln Leu Arg Asp Leu Tyr Leu Asn Gly Asp Phe Ala Ser Pro
            660                 665                 670

Ala Ser Asp Ala Thr Ala Pro Val Gln Ala Val Gly Lys Pro Glu Val
        675                 680                 685

Glu Tyr Asp Ile Phe Gly Glu Ala Ile Ala Ala Thr Ala Thr Val Glu
    690                 695                 700

Ile Pro Ala Ala Pro Ala Val Ala Pro Gln Tyr Gln Ser His Glu His
705                 710                 715                 720

Arg Phe Ala Arg Ala Ala Phe Asp Leu Trp Ala Thr His Leu Arg Asn
                725                 730                 735

Leu Ser Arg Arg Gln His Leu Leu Asp Leu Leu Glu Leu Pro Ala Glu
            740                 745                 750

Ala Ile Ala Leu Leu Val Lys Glu Leu Val Val Cys Ala Glu Arg Leu
        755                 760                 765

Asp Leu Pro Leu Gln Leu Ser Asn Ala Leu Leu Lys Arg Ala Gln Ser
    770                 775                 780

Gly Val Arg Lys Glu Asn Leu Val Gln Arg Gln Val Leu Thr Ala Gln
785                 790                 795                 800
```

-continued

```
Leu Leu Leu Asn Asp Phe Ala Ala Trp Phe Gly His Thr Ala Gln Pro
                805                 810                 815

Ala Gly Gln Arg Pro Thr Gly Leu Leu Gly Ala Lys Gln Pro Leu Phe
            820                 825                 830

Ala Phe Tyr Gln Lys Glu Met Pro Gly Arg Phe Pro His Leu Ala Ala
        835                 840                 845

Gln Ala Asp Asp Gln Ser Val Ile Phe Ala Asp Asp Trp Ile Ser Gly
    850                 855                 860

Ile Ala Ile His Thr Gln Lys Asn Val Gly His Arg Lys Gly Lys Glu
865                 870                 875                 880

Ile Thr Pro Glu Gln Asn Glu Ala Met Gly Arg Val Ile Gln Ala Phe
                885                 890                 895
Lys Ala Arg
```

<210> SEQ ID NO 57
<211> LENGTH: 795
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 57

```
atgaatataa atcgacaact gcctgtatca ggctcggagc gattgttgac tcccgacgtg     60

ggcgtatctc gccaggcttg ttccgaaagg cattattcta ctggacagga tcggcatgat    120

ttttaccgtt ttgctgccag gctacatgtg gatgcgcagt gttttggtct gtcaatagac    180

gatttgatgg ataagttttc tgacaagcac ttcagggctg agcatcctga atacagggat    240

gtctatccgg aggaatgttc tgccatttat atgcataccg ctcaagacta ttctagtcac    300

ctcgtaaggg gggaaatagg aacgccgctg taccgagagg tcaataatta tcttcgactt    360

caacatgaga attctgggcg agaagctgaa attgataatc acgacgaaaa gctatcgcct    420

cacataaaaa tgctttcatc tgcgcttaat cgtttaatgg atgtcgccgc ttttagagga    480

acggtttata gaggcattcg cggtgattta gataccattg ctcggctcta ccatctattc    540

gatacgggcg gccggtacgt agagcccgct ttcatgagta caactcgaat aaaggacagt    600

gcccaggtgt ttgagccagg cacgccaaac aacatagctt tccagataag cctaaaaaga    660

ggcgccgaca tttcgggatc ttcccaagcg ccctcagagg aagaaatcat gctacccatg    720

atgagtgagt tcgtcattga acatgcatcc gctctttccg aaggaaagca tttatttgta    780

ttaagtcaga tttga                                                     795
```

<210> SEQ ID NO 58
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 58

```
Met Asn Ile Asn Arg Gln Leu Pro Val Ser Gly Ser Glu Arg Leu Leu
  1               5                  10                  15

Thr Pro Asp Val Gly Val Ser Arg Gln Ala Cys Ser Glu Arg His Tyr
             20                  25                  30

Ser Thr Gly Gln Asp Arg His Asp Phe Tyr Arg Phe Ala Ala Arg Leu
         35                  40                  45

His Val Asp Ala Gln Cys Phe Gly Leu Ser Ile Asp Asp Leu Met Asp
     50                  55                  60

Lys Phe Ser Asp Lys His Phe Arg Ala Glu His Pro Glu Tyr Arg Asp
 65                  70                  75                  80
```

-continued

```
Val Tyr Pro Glu Glu Cys Ser Ala Ile Tyr Met His Thr Ala Gln Asp
                 85                  90                  95

Tyr Ser Ser His Leu Val Arg Gly Glu Ile Gly Thr Pro Leu Tyr Arg
            100                 105                 110

Glu Val Asn Asn Tyr Leu Arg Leu Gln His Glu Asn Ser Gly Arg Glu
        115                 120                 125

Ala Glu Ile Asp Asn His Asp Glu Lys Leu Ser Pro His Ile Lys Met
    130                 135                 140

Leu Ser Ser Ala Leu Asn Arg Leu Met Asp Val Ala Ala Phe Arg Gly
145                 150                 155                 160

Thr Val Tyr Arg Gly Ile Arg Gly Asp Leu Asp Thr Ile Ala Arg Leu
                165                 170                 175

Tyr His Leu Phe Asp Thr Gly Gly Arg Tyr Val Glu Pro Ala Phe Met
            180                 185                 190

Ser Thr Thr Arg Ile Lys Asp Ser Ala Gln Val Phe Glu Pro Gly Thr
        195                 200                 205

Pro Asn Asn Ile Ala Phe Gln Ile Ser Leu Lys Arg Gly Ala Asp Ile
    210                 215                 220

Ser Gly Ser Ser Gln Ala Pro Ser Glu Glu Glu Ile Met Leu Pro Met
225                 230                 235                 240

Met Ser Glu Phe Val Ile Glu His Ala Ser Ala Leu Ser Glu Gly Lys
                245                 250                 255

His Leu Phe Val Leu Ser Gln Ile
            260
```

<210> SEQ ID NO 59
<211> LENGTH: 897
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 59

```
atgaatatca gtcctgtatc gggtgcccac ggtagcagct acccttcagc tcaatccaca     60

gcatcgacgg catcgaaagg tccctctgga tcctttctca aacagctcgg cggctgtttt    120

tcaccctgcc tgggtagcag ctctactggg gccatacttt ctcccgctca tgagcaggta    180

ttgagccaca cctattccag caatattaaa ggaaagttgc gcacgacgcc cccaaaagga    240

ccgtcgccca ggttgtctga cacacctatg aagcaggcgc tttcttcaat gatcgtacag    300

gagcgaaaac ggcttaaaag tcaacccaag tcattggcct cggatataga acgtccagac    360

agtatgatca aaaaagcgct tgatgaaaaa gacggccacc cgtttggcga gcgcttttca    420

gacgacgaat ttcttgcgat tcatctctat acgagctgtc tttataggcc gatcaatcat    480

catctgcggt atgccccgaa caatgatgtt gcaccggttg tcgaggcact gaaaagtggt    540

ttggcaaagc ttgctcaaga ccctgattat caagtgtcta gccagcttca tagaggcatc    600

aagcaaaaga tgagtgatgg cgaggtcatg agtcgtttca aaccgggtaa gacctatcgt    660

gatgaagcgt tcatgagcac atcaactcat atgcaggttt cagaagagtt tacctccgac    720

gttacgttgc acctgcggtc ctcatcagct gtcaatatag gcccctttc gaaaaatcca    780

tacgaggacg aagcgcttat ctcgcccctg acgcctttca aagtaaccgg tctgcgcaag    840

caggacgata agtggcacgt cgatttgaac gagatagcag ataattcaga cgagtga       897
```

<210> SEQ ID NO 60
<211> LENGTH: 298
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 60

Met Asn Ile Ser Pro Val Ser Gly Ala His Gly Ser Ser Tyr Pro Ser
1 5 10 15

Ala Gln Ser Thr Ala Ser Thr Ala Ser Lys Gly Pro Ser Gly Ser Phe
20 25 30

Leu Lys Gln Leu Gly Gly Cys Phe Ser Pro Cys Leu Gly Ser Ser Ser
35 40 45

Thr Gly Ala Ile Leu Ser Pro Ala His Glu Gln Val Leu Ser His Thr
50 55 60

Tyr Ser Ser Asn Ile Lys Gly Lys Leu Arg Thr Thr Pro Pro Lys Gly
65 70 75 80

Pro Ser Pro Arg Leu Ser Asp Thr Pro Met Lys Gln Ala Leu Ser Ser
85 90 95

Met Ile Val Gln Glu Arg Lys Arg Leu Lys Ser Gln Pro Lys Ser Leu
100 105 110

Ala Ser Asp Ile Glu Arg Pro Asp Ser Met Ile Lys Lys Ala Leu Asp
115 120 125

Glu Lys Asp Gly His Pro Phe Gly Glu Arg Phe Ser Asp Asp Glu Phe
130 135 140

Leu Ala Ile His Leu Tyr Thr Ser Cys Leu Tyr Arg Pro Ile Asn His
145 150 155 160

His Leu Arg Tyr Ala Pro Asn Asn Asp Val Ala Pro Val Val Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Lys Leu Ala Gln Asp Pro Asp Tyr Gln Val
180 185 190

Ser Ser Gln Leu His Arg Gly Ile Lys Gln Lys Met Ser Asp Gly Glu
195 200 205

Val Met Ser Arg Phe Lys Pro Gly Lys Thr Tyr Arg Asp Glu Ala Phe
210 215 220

Met Ser Thr Ser Thr His Met Gln Val Ser Glu Glu Phe Thr Ser Asp
225 230 235 240

Val Thr Leu His Leu Arg Ser Ser Ser Ala Val Asn Ile Gly Pro Phe
245 250 255

Ser Lys Asn Pro Tyr Glu Asp Glu Ala Leu Ile Ser Pro Leu Thr Pro
260 265 270

Phe Lys Val Thr Gly Leu Arg Lys Gln Asp Asp Lys Trp His Val Asp
275 280 285

Leu Asn Glu Ile Ala Asp Asn Ser Asp Glu
290 295

<210> SEQ ID NO 61
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 61

atgaatatta acccttccct gggcgctcat ggcagcgcct actcgtcgcc tcaaagtgat 60

acttcgaagg ccactggaaa agcacctgcg ccttcttttt tcaaacagtt gggcggctgt 120

ttttcgccgt gccttggttc ccatgcgtca agcagccaac aactgtccgc cagtcatgcg 180

cagacgctca gtcagaatta ctccagcaac attcagggga cgagccgcac acgccagccg 240

agagcaccct cgccacgcct gtcagatacg cccatgaagc aggcgctttc ctcaatgatc 300

gaacgcgagc gtttgcggct tcaaggtctt tcgggaggaa tgttctcggg cattgactcc 360

-continued

gccgatgcca tgattggtcg agcgctcacg aagaaggatt caaacccaaa ggctgcgcgt 420

tttagtgatg atgagtttct cgccgttcac ctctacacaa cttgcctcta cagacctatc 480

aatcatcatc ttcggtatca acactag 507

<210> SEQ ID NO 62
<211> LENGTH: 168
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 62

Met Asn Ile Asn Pro Ser Leu Gly Ala His Gly Ser Ala Tyr Ser Ser
1 5 10 15

Pro Gln Ser Asp Thr Ser Lys Ala Thr Gly Lys Ala Pro Ala Pro Ser
20 25 30

Phe Phe Lys Gln Leu Gly Gly Cys Phe Ser Pro Cys Leu Gly Ser His
35 40 45

Ala Ser Ser Ser Gln Gln Leu Ser Ala Ser His Ala Gln Thr Leu Ser
50 55 60

Gln Asn Tyr Ser Ser Asn Ile Gln Gly Thr Ser Arg Thr Arg Gln Pro
65 70 75 80

Arg Ala Pro Ser Pro Arg Leu Ser Asp Thr Pro Met Lys Gln Ala Leu
85 90 95

Ser Ser Met Ile Glu Arg Glu Arg Leu Arg Leu Gln Gly Leu Ser Gly
100 105 110

Gly Met Phe Ser Gly Ile Asp Ser Ala Asp Ala Met Ile Gly Arg Ala
115 120 125

Leu Thr Lys Lys Asp Ser Asn Pro Lys Ala Ala Arg Phe Ser Asp Asp
130 135 140

Glu Phe Leu Ala Val His Leu Tyr Thr Thr Cys Leu Tyr Arg Pro Ile
145 150 155 160

Asn His His Leu Arg Tyr Gln His
165

<210> SEQ ID NO 63
<211> LENGTH: 2823
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 63

atgagctcga tcacgcacac caacacgccg caattggcgg tcagcgattc acggggtctg 60

ccggtacgca gtgtgcagtt ctatcgtggc gctgatggtc agcctgttga cgcgagggtg 120

acgcagcact atttcgacaa ggccgggcga ctgatcgcca gtcgcgatcc acgtttttcc 180

agtcgtttga aatacggtgt ctgtgcgcct gtgaacctga tgcaaatcgt cagcttgtcc 240

ggggctttgc tgttatcgaa aagtgtcgat tcaggttggc gggtgagcct gaacggcgaa 300

gcggggcagt tagtcgacag ctgtgacgga cgtgacaacc cgcgccagat cgaatacgac 360

gggctgttgc gccctttggc gatcaacgaa tcaggccgaa tgaccgagcg cttcacttat 420

ggcgggcctg ccactgctga gcataaccag tgcaatcaac tgattcgcca tgacgatacg 480

gcaggctcgc gcttgctgcg ggactatgga ctgtcgggta gggcgttgag cgaaaaaagg 540

tacttcctgc agtcgcccga cagcccggac tggccacttg ccgagcctga tcgtgatgca 600

ctgctcgagc cggtcggcct gcagacgcgc tgggctttca acgcgcaggg cgaggacctg 660

gcgcagactg acgcaaacgg taatgtccag cgtttcagtc acggtgtggc tgggcaactg 720

-continued

cacgctgttg aactgaccct ggccaatacg gcacagcggc aaacgctggt cagtgcaatt 780

cactacgacg cgttcaatca ggccgagcag gagacggcag gaaatggtgt ggtcagtcgc 840

tatgtgtatg atcaacagga cggtcggctg actgagctca gtgcgctatc tgccgacggc 900

tcagtgttgc aaaaactgaa ctacagctat gacccggcag gtaacgttct actcatcaac 960

gatgcctcgc aaccagaccg gtattgcggc aatcagcgta tcgagccgat aaaccgttac 1020

tgttacgaca cgttgtatca gttgatcgaa gccacggggc gggaggtcag aaacggggcc 1080

agccatggtc cggcgctacc cggtctgcaa cctctgccga cgctcgatcc ttgccaggtc 1140

agcaactaca cacagcgtta cagctacgac gctgcgggta acctgctgca aatgcgccac 1200

gaaggcgcgc acaacttcac ccgcaacatg cacgttgatc ccgacagcaa tcgcagcctg 1260

cccgacaatg acaggtatgt ggatttcgcc acgagttttg atgccaacgg caatctgctg 1320

caactcgtgc gtgggcagac catgagctgg gatgtgcgta atcagttgcg gcaaatcact 1380

accgtgcaac gtgaagacgc accgaatgat gaagagcgct atgtatacga cggccagggc 1440

cagcgctgcc gcaagatcag caccgcgcag gcatcaggtc gcacactgac caatgaagtt 1500

cgctacctgc cgggactgga agttcggacc acggccgatg gagaaactct tcacgtcgtt 1560

acggctcagg cgggtcgcaa cagcgtgcgg gtgttgcact gggaagccgg aaaaccaggc 1620

gctattgcga acgatcaggt gcgttacagc ctgggtgatc atctgggctc gagcacgctg 1680

gagcttgatc agcaaggcgg cctgatcagc caggaaagtt attacccctt tggcggcacg 1740

gcctggtggg cggcgcgtag tgcagtggag gccaagtaca aaacagtgcg ttattcgggt 1800

aaagagcgcg atgccagcgg gctttattat tacgggttca ggtattacgc gccgtggttg 1860

cagcggtgga tcaatcctga cccggcgggg gatgtggatg ggttgaatct gtacaggatg 1920

gtcagaaata atccgcttgt ttacgttgat gcgaagggcc agcaacctga acctgttcca 1980

aaaactattc accagatctg gataggtgaa aacaagaatg ccttgagagc tcaggttagc 2040

aatatcaaca gaaccgttga aatggcttgg gggtataaag tgaagttgca tctggaaacg 2100

aggacgccgg aagcttattc ggaaatcgaa aaggatctga gatccgaagt ggttctgctt 2160

cctgattccc aggtttttca aaacttcaag gagaagccgc tttatgcggc ctatgaagat 2220

ttccgaagaa acaatcagaa ttacgctttc gcggtagacg ttttacgtat gcataccgtt 2280

catgagttgg gcgggattta ttcagatgtc gatgacgttt atgcaggtgc ggagactggc 2340

ggaatgacgc agttgggggа taatccgctg tttgcagaac ctgatgaggt tttgacgctg 2400

gatcctgttc atgtcccttg ggagccccag aattctgttg aaagttttat ggtcaataac 2460

agctcatttg ccgctcattc aggtgcaggc gtcttacttg acatgatggg ggaaggagcg 2520

aaacgatatg atgaagccgt tgagggcgga agttatccgg atccgacggg catgaacggt 2580

ataggtctaa gtctgctctg gaatcctaac ccggcagtaa gagttcgaac gttatcgaat 2640

gtagtaggcc ccggcttgtt tacagacaca ctgcacgctt cggacacagc atacggtgag 2700

ctttttagta atctgaaagg cgtcgtcttt caaaaacagc cgttcacgtt tgccgaccaa 2760

atggccagga agatgccgct gcatcggcat ataaaaagcg gcgcggcgca aacctggcgc 2820

tga 2823

<210> SEQ ID NO 64
<211> LENGTH: 940
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 64

```
Met Ser Ser Ile Thr His Thr Asn Thr Pro Gln Leu Ala Val Ser Asp
  1               5                  10                  15

Ser Arg Gly Leu Pro Val Arg Ser Val Gln Phe Tyr Arg Gly Ala Asp
             20                  25                  30

Gly Gln Pro Val Asp Ala Arg Val Thr Gln His Tyr Phe Asp Lys Ala
         35                  40                  45

Gly Arg Leu Ile Ala Ser Arg Asp Pro Arg Phe Ser Ser Arg Leu Lys
     50                  55                  60

Tyr Gly Val Cys Ala Pro Val Asn Leu Met Gln Ile Val Ser Leu Ser
 65                  70                  75                  80

Gly Ala Leu Leu Leu Ser Lys Ser Val Asp Ser Gly Trp Arg Val Ser
                 85                  90                  95

Leu Asn Gly Glu Ala Gly Gln Leu Val Asp Ser Cys Asp Gly Arg Asp
            100                 105                 110

Asn Pro Arg Gln Ile Glu Tyr Asp Gly Leu Leu Arg Pro Leu Ala Ile
        115                 120                 125

Asn Glu Ser Gly Arg Met Thr Glu Arg Phe Thr Tyr Gly Gly Pro Ala
    130                 135                 140

Thr Ala Glu His Asn Gln Cys Asn Gln Leu Ile Arg His Asp Asp Thr
145                 150                 155                 160

Ala Gly Ser Arg Leu Leu Arg Asp Tyr Gly Leu Ser Gly Arg Ala Leu
                165                 170                 175

Ser Glu Lys Arg Tyr Phe Leu Gln Ser Pro Asp Ser Pro Asp Trp Pro
            180                 185                 190

Leu Ala Glu Pro Asp Arg Asp Ala Leu Leu Glu Pro Val Gly Leu Gln
        195                 200                 205

Thr Arg Trp Ala Phe Asn Ala Gln Gly Glu Asp Leu Ala Gln Thr Asp
    210                 215                 220

Ala Asn Gly Asn Val Gln Arg Phe Ser His Gly Val Ala Gly Gln Leu
225                 230                 235                 240

His Ala Val Glu Leu Thr Leu Ala Asn Thr Ala Gln Arg Gln Thr Leu
                245                 250                 255

Val Ser Ala Ile His Tyr Asp Ala Phe Asn Gln Ala Glu Gln Glu Thr
            260                 265                 270

Ala Gly Asn Gly Val Val Ser Arg Tyr Val Tyr Asp Gln Gln Asp Gly
        275                 280                 285

Arg Leu Thr Glu Leu Ser Ala Leu Ser Ala Asp Gly Ser Val Leu Gln
    290                 295                 300

Lys Leu Asn Tyr Ser Tyr Asp Pro Ala Gly Asn Val Leu Leu Ile Asn
305                 310                 315                 320

Asp Ala Ser Gln Pro Asp Arg Tyr Cys Gly Asn Gln Arg Ile Glu Pro
                325                 330                 335

Ile Asn Arg Tyr Cys Tyr Asp Thr Leu Tyr Gln Leu Ile Glu Ala Thr
            340                 345                 350

Gly Arg Glu Val Arg Asn Gly Ala Ser His Gly Pro Ala Leu Pro Gly
        355                 360                 365

Leu Gln Pro Leu Pro Thr Leu Asp Pro Cys Gln Val Ser Asn Tyr Thr
    370                 375                 380

Gln Arg Tyr Ser Tyr Asp Ala Ala Gly Asn Leu Leu Gln Met Arg His
385                 390                 395                 400

Glu Gly Ala His Asn Phe Thr Arg Asn Met His Val Asp Pro Asp Ser
                405                 410                 415
```

-continued

```
Asn Arg Ser Leu Pro Asp Asn Asp Arg Tyr Val Asp Phe Ala Thr Ser
            420                 425                 430

Phe Asp Ala Asn Gly Asn Leu Leu Gln Leu Val Arg Gly Gln Thr Met
        435                 440                 445

Ser Trp Asp Val Arg Asn Gln Leu Arg Gln Ile Thr Thr Val Gln Arg
    450                 455                 460

Glu Asp Ala Pro Asn Asp Glu Glu Arg Tyr Val Tyr Asp Gly Gln Gly
465                 470                 475                 480

Gln Arg Cys Arg Lys Ile Ser Thr Ala Gln Ala Ser Gly Arg Thr Leu
                485                 490                 495

Thr Asn Glu Val Arg Tyr Leu Pro Gly Leu Glu Val Arg Thr Thr Ala
            500                 505                 510

Asp Gly Glu Thr Leu His Val Val Thr Ala Gln Ala Gly Arg Asn Ser
        515                 520                 525

Val Arg Val Leu His Trp Glu Ala Gly Lys Pro Gly Ala Ile Ala Asn
    530                 535                 540

Asp Gln Val Arg Tyr Ser Leu Gly Asp His Leu Gly Ser Ser Thr Leu
545                 550                 555                 560

Glu Leu Asp Gln Gln Gly Gly Leu Ile Ser Gln Glu Ser Tyr Tyr Pro
                565                 570                 575

Phe Gly Gly Thr Ala Trp Trp Ala Ala Arg Ser Ala Val Glu Ala Lys
            580                 585                 590

Tyr Lys Thr Val Arg Tyr Ser Gly Lys Glu Arg Asp Ala Ser Gly Leu
        595                 600                 605

Tyr Tyr Tyr Gly Phe Arg Tyr Tyr Ala Pro Trp Leu Gln Arg Trp Ile
    610                 615                 620

Asn Pro Asp Pro Ala Gly Asp Val Asp Gly Leu Asn Leu Tyr Arg Met
625                 630                 635                 640

Val Arg Asn Asn Pro Leu Val Tyr Val Asp Ala Lys Gly Gln Gln Pro
                645                 650                 655

Glu Pro Val Pro Lys Thr Ile His Gln Ile Trp Ile Gly Glu Asn Lys
            660                 665                 670

Asn Ala Leu Arg Ala Gln Val Ser Asn Ile Asn Arg Thr Val Glu Met
        675                 680                 685

Ala Trp Gly Tyr Lys Val Lys Leu His Leu Glu Thr Arg Thr Pro Glu
    690                 695                 700

Ala Tyr Ser Glu Ile Glu Lys Asp Leu Arg Ser Glu Val Val Leu Leu
705                 710                 715                 720

Pro Asp Ser Gln Val Phe Gln Asn Phe Lys Glu Lys Pro Leu Tyr Ala
                725                 730                 735

Ala Tyr Glu Asp Phe Arg Arg Asn Asn Gln Asn Tyr Ala Phe Ala Val
            740                 745                 750

Asp Val Leu Arg Met His Thr Val His Glu Leu Gly Gly Ile Tyr Ser
        755                 760                 765

Asp Val Asp Asp Val Tyr Ala Gly Ala Glu Thr Gly Gly Met Thr Gln
    770                 775                 780

Leu Gly Asp Asn Pro Leu Phe Ala Glu Pro Asp Glu Val Leu Thr Leu
785                 790                 795                 800

Asp Pro Val His Val Pro Trp Glu Pro Gln Asn Ser Val Glu Ser Phe
                805                 810                 815

Met Val Asn Asn Ser Ser Phe Ala Ala His Ser Gly Ala Gly Val Leu
            820                 825                 830
```

-continued

```
Leu Asp Met Met Gly Glu Gly Ala Lys Arg Tyr Asp Glu Ala Val Glu
        835                 840                 845

Gly Gly Ser Tyr Pro Asp Pro Thr Gly Met Asn Gly Ile Gly Leu Ser
    850                 855                 860

Leu Leu Trp Asn Pro Asn Pro Ala Val Arg Val Arg Thr Leu Ser Asn
865                 870                 875                 880

Val Val Gly Pro Gly Leu Phe Thr Asp Thr Leu His Ala Ser Asp Thr
                885                 890                 895

Ala Tyr Gly Glu Leu Phe Ser Asn Leu Lys Gly Val Val Phe Gln Lys
            900                 905                 910

Gln Pro Phe Thr Phe Ala Asp Gln Met Ala Arg Lys Met Pro Leu His
        915                 920                 925

Arg His Ile Lys Ser Gly Ala Ala Gln Thr Trp Arg
    930                 935                 940


<210> SEQ ID NO 65
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 65

atgccgatca ccgcgcagca gttgctgcag atactcccga gcgctggcca gaaagccggc     60

gtttttgcac ccgtcctgaa cacagcgatg agcaagcacc agatcttgac gccgctgcgc    120

atcgcggctt tcatcgccca ggtcggtcat gagtccggcc aactgcgcta cgtccgcgag    180

atttgggggc cgactccgca gcagctgggt tatgaaggcc gcaaggacct cggcaatacc    240

gtggcgggtg atggttcgaa gtaccgcggg cgcggcctga tccagatcac cggccgggcc    300

aactatgccg aatgcggcga ggcgctgggc ctagacctga tccatcaccc ggaactgctc    360

gagcagccgg agcacgccac aatgtcggca gcgtggtact ggagcagccg tggcctgaac    420

tcgctggccg acaaagggga ctttcttcaa attacccgaa gaatcaacgg aggcaccaat    480

ggactggcgg atcggcaggc gctgtacgac cgggcgctga aggtgctggc gtga          534


<210> SEQ ID NO 66
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 66

Met Pro Ile Thr Ala Gln Gln Leu Leu Gln Ile Leu Pro Ser Ala Gly
  1               5                  10                  15

Gln Lys Ala Gly Val Phe Ala Pro Val Leu Asn Thr Ala Met Ser Lys
             20                  25                  30

His Gln Ile Leu Thr Pro Leu Arg Ile Ala Ala Phe Ile Ala Gln Val
         35                  40                  45

Gly His Glu Ser Gly Gln Leu Arg Tyr Val Arg Glu Ile Trp Gly Pro
     50                  55                  60

Thr Pro Gln Gln Leu Gly Tyr Glu Gly Arg Lys Asp Leu Gly Asn Thr
 65                  70                  75                  80

Val Ala Gly Asp Gly Ser Lys Tyr Arg Gly Arg Gly Leu Ile Gln Ile
                 85                  90                  95

Thr Gly Arg Ala Asn Tyr Ala Glu Cys Gly Glu Ala Leu Gly Leu Asp
            100                 105                 110

Leu Ile His His Pro Glu Leu Leu Glu Gln Pro Glu His Ala Thr Met
        115                 120                 125
```

-continued

```
Ser Ala Ala Trp Tyr Trp Ser Ser Arg Gly Leu Asn Ser Leu Ala Asp
    130                 135                 140

Lys Gly Asp Phe Leu Gln Ile Thr Arg Arg Ile Asn Gly Gly Thr Asn
145                 150                 155                 160

Gly Leu Ala Asp Arg Gln Ala Leu Tyr Asp Arg Ala Leu Lys Val Leu
                165                 170                 175
Ala
```

<210> SEQ ID NO 67
<211> LENGTH: 1137
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 67

```
atgaatctaa cagctttagg ttcaaagctg tctcggtatc gcaagcagct tgcgatgagc     60

gaggaagaag tgtgtgcggt cacccacatc ccccttgagc gcctgcagtc agttgaagcc    120

ggctctcagg cgcctacggg tgatgaagtg cttatcctgg ccgatctcta ccactgcaac    180

ttcaaattct tcatctcgaa cgagccgctc gccccctttg agcagaccga aatcctgtat    240

cgcaggcacg gagctgagtt catcaaggag gatcgtagag ccgtccaaga attcctgtac    300

ctctgcgaaa cagaggactt cctgatgagt gagttgaagg ctatgaagct cgaatttccg    360

ctgccgcagg cttctgggaa ttttaagaat gatggaatcc gagcggctga agcctttcgc    420

cttttcaatc agcaccccac aaacgccgtg cctcgggatg tgtatcagga gattcgccaa    480

accggagtgc atgtgttccg tagaaagctt ggtaactcta acatttcggg gcttttcctg    540

gctcacccca cggctgggaa gtgcattctg gtcaactaca gcgaagacgt ataccggcag    600

cggtttagcg ctgcgcatga atttgctcac gctcttttcg atgcgcaggg tggccccagt    660

attacctact cccgtacgac taaggctgac ctagtcgaag tgagagcaaa caccttgcc     720

tcccggtatc tgatgccttc agaaatcctc cgacagctgc ccaaccctga gcaatggaca    780

caggaaaata cccagtattg ggctcatgag ttgcgagtca gctgcgttgc cttgggcata    840

ggtctgaagt ccgagggctt aattagcgag caagcattcc agaggataaa gtcgtaccgc    900

gttcctcgtg aactgaagat tgacccagaa ttgccggccc aattgacgac gcaacagcgt    960

gagcgaaagg ctaagttact ggaaaagggg ttatctgaca gctacgtcgc actgtgccta   1020

gacgctcaga gccgtggcat catcactcaa ggtcgattgg ctgaagcctt gcttagtgac   1080

ttgggaggcc ttcaagagct gctcagcctt tatggaagat cgcgcaatgg ccattga      1137
```

<210> SEQ ID NO 68
<211> LENGTH: 378
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 68

```
Met Asn Leu Thr Ala Leu Gly Ser Lys Leu Ser Arg Tyr Arg Lys Gln
  1               5                  10                  15

Leu Ala Met Ser Glu Glu Glu Val Cys Ala Val Thr His Ile Pro Leu
             20                  25                  30

Glu Arg Leu Gln Ser Val Glu Ala Gly Ser Gln Ala Pro Thr Gly Asp
         35                  40                  45

Glu Val Leu Ile Leu Ala Asp Leu Tyr His Cys Asn Phe Lys Phe Phe
     50                  55                  60

Ile Ser Asn Glu Pro Leu Ala Pro Phe Glu Gln Thr Glu Ile Leu Tyr
 65                  70                  75                  80
```

-continued

```
Arg Arg His Gly Ala Glu Phe Ile Lys Glu Asp Arg Arg Ala Val Gln
                 85                  90                  95

Glu Phe Leu Tyr Leu Cys Glu Thr Glu Asp Phe Leu Met Ser Glu Leu
            100                 105                 110

Lys Ala Met Lys Leu Glu Phe Pro Leu Pro Gln Ala Ser Gly Asn Phe
        115                 120                 125

Lys Asn Asp Gly Ile Arg Ala Ala Glu Ala Phe Arg Leu Phe Asn Gln
    130                 135                 140

His Pro Thr Asn Ala Val Pro Arg Asp Val Tyr Gln Glu Ile Arg Gln
145                 150                 155                 160

Thr Gly Val His Val Phe Arg Arg Lys Leu Gly Asn Ser Asn Ile Ser
                165                 170                 175

Gly Leu Phe Leu Ala His Pro Thr Ala Gly Lys Cys Ile Leu Val Asn
            180                 185                 190

Tyr Ser Glu Asp Val Tyr Arg Gln Arg Phe Ser Ala Ala His Glu Phe
        195                 200                 205

Ala His Ala Leu Phe Asp Ala Gln Gly Gly Pro Ser Ile Thr Tyr Ser
    210                 215                 220

Arg Thr Thr Lys Ala Asp Leu Val Glu Val Arg Ala Asn Thr Phe Ala
225                 230                 235                 240

Ser Arg Tyr Leu Met Pro Ser Glu Ile Leu Arg Gln Leu Pro Asn Pro
                245                 250                 255

Glu Gln Trp Thr Gln Glu Asn Thr Gln Tyr Trp Ala His Glu Leu Arg
            260                 265                 270

Val Ser Cys Val Ala Leu Gly Ile Gly Leu Lys Ser Glu Gly Leu Ile
        275                 280                 285

Ser Glu Gln Ala Phe Gln Arg Ile Lys Ser Tyr Arg Val Pro Arg Glu
    290                 295                 300

Leu Lys Ile Asp Pro Glu Leu Pro Ala Gln Leu Thr Thr Gln Gln Arg
305                 310                 315                 320

Glu Arg Lys Ala Lys Leu Leu Glu Lys Gly Leu Ser Asp Ser Tyr Val
                325                 330                 335

Ala Leu Cys Leu Asp Ala Gln Ser Arg Gly Ile Ile Thr Gln Gly Arg
            340                 345                 350

Leu Ala Glu Ala Leu Leu Ser Asp Leu Gly Gly Leu Gln Glu Leu Leu
        355                 360                 365

Ser Leu Tyr Gly Arg Ser Arg Asn Gly His
    370                 375
```

<210> SEQ ID NO 69
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 69

```
atgaatatca acccttggc ttcttcatta cagaatcaac agcgcactct cttaggcccg     60

ccccccctca attcatctgc tgctctgccg atcaagatcc ctgtggcgca tgataaagcg    120

cgtgacccta acgctgaatt ctataccacc gaggaaacgc cctggtttgc cggctacaaa    180

aagtcggagg caggacgcgc tattttagag aaaatgtctg agaaggaagc aaaagatatc    240

cgaggcgagt atctgggaaa ctacatgaaa gcctttgacg aaaccatatg tcgtatgtac    300

gacaattttc acgatttcaa acagcagctt ttttacctta atacggagct gtcaaaaaag    360

catttcggct tcacgctggg ctttaatcag gacattcagg tgaccgaccc ggacgaggta    420
```

-continued

```
ctcaccccgg cagagttcac gtacctgacc gagaagctga acgaacgcca acaactgaaa    480

gaggatctgc gtgcgcacgc aaaaattgtg atgacgctgc tcgaccatta caccgaaaaa    540

ttcgataacc ggcacaccct caatctggag agttacagca aggtcatcga ctacggacag    600

atcttcagcc gcaatcatat tggcaatttc atggacacga ttatctacca gatcgagcgc    660

aatgcgccga agcgtgagga agaaccaaaa cctctggttg atgtgcacgc ttga          714


<210> SEQ ID NO 70
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 70

Met Asn Ile Asn Pro Leu Ala Ser Ser Leu Gln Asn Gln Gln Arg Thr
  1               5                  10                  15

Leu Leu Gly Pro Pro Pro Leu Asn Ser Ser Ala Ala Leu Pro Ile Lys
             20                  25                  30

Ile Pro Val Ala His Asp Lys Ala Arg Asp Pro Asn Ala Glu Phe Tyr
         35                  40                  45

Thr Thr Glu Glu Thr Pro Trp Phe Ala Gly Tyr Lys Lys Ser Glu Ala
     50                  55                  60

Gly Arg Ala Ile Leu Glu Lys Met Ser Glu Lys Glu Ala Lys Asp Ile
 65                  70                  75                  80

Arg Gly Glu Tyr Leu Gly Asn Tyr Met Lys Ala Phe Asp Glu Thr Ile
                 85                  90                  95

Cys Arg Met Tyr Asp Asn Phe His Asp Phe Lys Gln Gln Leu Phe Tyr
            100                 105                 110

Leu Asn Thr Glu Leu Ser Lys Lys His Phe Gly Phe Thr Leu Gly Phe
        115                 120                 125

Asn Gln Asp Ile Gln Val Thr Asp Pro Asp Glu Val Leu Thr Pro Ala
    130                 135                 140

Glu Phe Thr Tyr Leu Thr Glu Lys Leu Asn Glu Arg Gln Gln Leu Lys
145                 150                 155                 160

Glu Asp Leu Arg Ala His Ala Lys Ile Val Met Thr Leu Leu Asp His
                165                 170                 175

Tyr Thr Glu Lys Phe Asp Asn Arg His Thr Leu Asn Leu Glu Ser Tyr
            180                 185                 190

Ser Lys Val Ile Asp Tyr Gly Gln Ile Phe Ser Arg Asn His Ile Gly
        195                 200                 205

Asn Phe Met Asp Thr Ile Ile Tyr Gln Ile Glu Arg Asn Ala Pro Lys
    210                 215                 220

Arg Glu Glu Glu Pro Lys Pro Leu Val Asp Val His Ala
225                 230                 235


<210> SEQ ID NO 71
<211> LENGTH: 3693
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 71

atgggcctga tcggcgtcaa acagaacaaa ccgcaacagg cgcagaccta cctgacgcgc     60

ctgcaagcgc tgtcgccagc gccctggcag gcggtgcagc tggagcagga cattgccctc    120

ggccagccgc aaaatcaggc gctgctggat gatgcccgac gcctggccga cgccggtgag    180

cgtgacaagg cgaccggggt gtttcgccag ttgttcaacg gccgtttgcc tcaaggcact    240
```

-continued

```
gtcggccgcg agtactacac caacctgggc ttcaacaatg cggactggcc cgaggcgcgc    300
aagggttttg aacgcctgat gcggcagaac cctgacgact cgattctggc gctgttcttt    360
gccaagcacc tggcccgccg cgaagacagc cgcgccgaag gcatcgccgc tctggcgcgc    420
ctgagcactc atccggacat cgccggcgat gccgatcaga gctggcgcat ggcgctggtc    480
tggatcggcc cgcctgcggc tgcgcaagtg ccactgttcg acgcgtttct caaggttcat    540
cccgacgatc aggaaatccg cgaccagttg aacaagggtc gccagcagca tgccagcggc    600
gctgcctcag gctggcagca agacccgctg gtggcgcgcg gcttgaaggc gctggaaaaa    660
aatgatcatg tggcggccga agaagccttt gccgcccgcc tgaaaatcaa ggcggacgat    720
gccaacgtgc ttggcggcct gggcgtggtg cgtcagcagc agaaccggtt gcctgaagcc    780
gaacaattgc tgacccgcgc cacgcgccag cagggcggtg cgcgctggaa aaacgcgctg    840
gaaaacgtac agctctggac ctcgctgcaa gaggcccgtg acctgcaggc caaagggcag    900
accggcaagg ctcaagcgtt gctggctcag gcgcagcggc aaaaccctga caatatcgac    960
gtgcgtttga ccctggccga cgtgcaggtg caggccgggc aactggacgc cgcgcaagcg   1020
ggctatcgtc aggtactggc gacccagcgc ggtaatccgc aggcaatccg cgggctgatc   1080
aacgtgctgg cccagcgtgg tcaggctgat gaagcgttgc gcctgctcga cacattgtcg   1140
ccaggcgaac aggccaaact gggcgacagc ggtcgcttca aggcgctgcg ctccacccag   1200
gtggcgcggc tggccgagca gcgtggcgat gttcgcgctg cccaggtggc cttgaaagac   1260
gcggtgaaga acgacccgga caatgtctgg acgcgttttg atctggcgcg cctgtacctc   1320
aagaccgacg aagcgcccaa ggcccgcgcg ctgatcgacg agctgctcaa ggctcagccc   1380
aacaatatcg atgcgctcta caccagcgcg ctgctgtcag tggaaatggg ccagtggcag   1440
gacgcgcaga ccacgtttac gcgcatcccg gttgatcagc gcacgccgga catgaaagcg   1500
cttgctgacg aagtcaccat gaccgtgcag atcaatctgg ccatcggcat cgcccggcgc   1560
ggtcagcgcc aggaagcgtt ggcgctgctc gatcgcttgc aaccggtcgc cagcggcagc   1620
ccggagcgtc aactcacgct ggccagcgct tacatcgatg cgggcgagcc cgcgcgcggt   1680
cgggaaatgg cccgtgcggc catcgctcag gcccctttgc cgtcggccga cctgatgctg   1740
caatacgccg gtctgctgct cgcagcgggc gatgacgtgc aggtcaatgc gatcctgcgc   1800
aacgtgcagg gtcagccgat gagcgtgcag acccgcaaac gttttgatga ccttttgtac   1860
cgctaccgca ttcgtcaggc cgatctgctg cgtgaaggcg gtgatctggc gggcgcgtac   1920
gacacgctgg cacctgcttt ggcgcagcgc ccggacgaca ttcaggcggt gtcggccttc   1980
gcccgcatgt acaccgccaa tggcgacagc gcccgagcgt tcgagctgta caagcctttg   2040
ttgcagcgcc agcccaatga cccgcaagtg ttgctgggcg cagccgatgc ggcggtcaaa   2100
gcgcatgatt atggctttgc cgaaaaagcc ctgagccagt tccgcaaact ggagcgtaac   2160
gacccgcaga ccctgacgga ggccgcacgt atctaccaaa gcatggggca gaccggcgcg   2220
gccaccgagt tgctgcgcaa ggccgtggcc atcgaacaga gtgaaaaaca gcgcgcgatg   2280
gctgtgcagg ctgtgtcgac cagcaccacg tcgtccaacc cgtttgcgac gggcggctca   2340
cgtagcctgg cggcggcttc ggctattccg gctccggctc aggtgtcgct cagcggtggg   2400
agagcgcttg aaacaaacag tgcgcctgaa atatctgccc cgcgtgacac cgcttatccc   2460
ggccagatcg ccgcaccaca accgctgtct gccgcacgta cgcaaagtgt gcgcggcaat   2520
ccgttcatgg cagccaccga ccgcgatcag gccagcagcg cacagcaggc gctcaatcgc   2580
attcttgagc agcgcagtgg cttcgtcagt cagggcctgg ccgtgcgcag caataacagc   2640
```

-continued

```
gagtcgggtc tgagcaaact gaccgtggtc gagaccccgc tagaggtcaa tttgcctgcc   2700

ggtgataacc gggtggccgt gcgcgtcacg ccggtgtcgc tgaatgctgg cagcttgaag   2760

tcagatgcag gtgcccgttt tggcggtggc accagcggtg ctgccggttc gcagagcgac   2820

aagggtgtcg gtctggcggt ggcgttcgag cgccccgaag aaggcctcaa ggccgatatc   2880

ggcaccacgc cgatgggttt caaatacacc acggttgccg gcggcgcgag tgtcgaccgg   2940

ccgttgggta acaacccgga cctgcgctac ggcctcaacg tgtcacggcg tccggtgacg   3000

gacagcgtga cttcgtttgc cggttccaca gacgagcgca gcggcctgtc ctggggcggc   3060

gtcacggcca acggcgggcg cggtcagctc agctatgacg accagaccat cggcggttat   3120

ggctacggct cgtggcacaa actggttggc aacaacgtga aatccaacac ccgaggcgaa   3180

gtgggtggcg gcgtttactg gtacctgcgc aatgccgagg acagcaaact gaccgcaggc   3240

ctgagcctga tgggcatgag ctatgacaat gaccagagct acttcacgta cggccacggt   3300

ggctatttca gcccgcagag cttctatgcc atcggcgtgc cggtgatgtg ggcacagcgc   3360

accgagcgtt tcagctatca ggtcaagagc tcggtcgggg tccagcactt caagcaggac   3420

ggcgccgaat tcttccccga cgacagcacg ctacaggccg cttccgccca gcgctacaca   3480

gggcaaagca aaaccggaat tggctacaac ctgagcgcgg caggcgagta caagctcgat   3540

tccagcctgt tcatgggggc cagtctgggc ctggacaatg cccgggacta tcgccagttc   3600

agcggcgcgc tttacctgcg ttacatgttc gaggacataa ccggcccgat ggcactgccg   3660

gtcagccctt accgttcacc ttattccaac tga                               3693
```

<210> SEQ ID NO 72
<211> LENGTH: 1230
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 72

```
Met Gly Leu Ile Gly Val Lys Gln Asn Lys Pro Gln Gln Ala Gln Thr
  1               5                  10                  15

Tyr Leu Thr Arg Leu Gln Ala Leu Ser Pro Ala Pro Trp Gln Ala Val
             20                  25                  30

Gln Leu Glu Gln Asp Ile Ala Leu Gly Gln Pro Gln Asn Gln Ala Leu
         35                  40                  45

Leu Asp Asp Ala Arg Arg Leu Ala Asp Ala Gly Glu Arg Asp Lys Ala
     50                  55                  60

Thr Gly Val Phe Arg Gln Leu Phe Asn Gly Arg Leu Pro Gln Gly Thr
 65                  70                  75                  80

Val Gly Arg Glu Tyr Tyr Thr Asn Leu Gly Phe Asn Asn Ala Asp Trp
                 85                  90                  95

Pro Glu Ala Arg Lys Gly Phe Glu Arg Leu Met Arg Gln Asn Pro Asp
            100                 105                 110

Asp Ser Ile Leu Ala Leu Phe Phe Ala Lys His Leu Ala Arg Arg Glu
        115                 120                 125

Asp Ser Arg Ala Glu Gly Ile Ala Ala Leu Ala Arg Leu Ser Thr His
    130                 135                 140

Pro Asp Ile Ala Gly Asp Ala Asp Gln Ser Trp Arg Met Ala Leu Val
145                 150                 155                 160

Trp Ile Gly Pro Pro Ala Ala Ala Gln Val Pro Leu Phe Asp Ala Phe
                165                 170                 175

Leu Lys Val His Pro Asp Asp Gln Glu Ile Arg Asp Gln Leu Asn Lys
            180                 185                 190
```

-continued

```
Gly Arg Gln Gln His Ala Ser Gly Ala Ala Ser Gly Trp Gln Gln Asp
        195                 200                 205

Pro Leu Val Ala Arg Gly Leu Lys Ala Leu Glu Lys Asn Asp His Val
    210                 215                 220

Ala Ala Glu Glu Ala Phe Ala Ala Arg Leu Lys Ile Lys Ala Asp Asp
225                 230                 235                 240

Ala Asn Val Leu Gly Gly Leu Gly Val Val Arg Gln Gln Gln Asn Arg
                245                 250                 255

Leu Pro Glu Ala Glu Gln Leu Leu Thr Arg Ala Thr Arg Gln Gln Gly
            260                 265                 270

Gly Ala Arg Trp Lys Asn Ala Leu Glu Asn Val Gln Leu Trp Thr Ser
        275                 280                 285

Leu Gln Glu Ala Arg Asp Leu Gln Ala Lys Gly Gln Thr Gly Lys Ala
    290                 295                 300

Gln Ala Leu Leu Ala Gln Ala Gln Arg Gln Asn Pro Asp Asn Ile Asp
305                 310                 315                 320

Val Arg Leu Thr Leu Ala Asp Val Gln Val Gln Ala Gly Gln Leu Asp
                325                 330                 335

Ala Ala Gln Ala Gly Tyr Arg Gln Val Leu Ala Thr Gln Arg Gly Asn
            340                 345                 350

Pro Gln Ala Ile Arg Gly Leu Ile Asn Val Leu Ala Gln Arg Gly Gln
        355                 360                 365

Ala Asp Glu Ala Leu Arg Leu Leu Asp Thr Leu Ser Pro Gly Glu Gln
    370                 375                 380

Ala Lys Leu Gly Asp Ser Gly Arg Phe Lys Ala Leu Arg Ser Thr Gln
385                 390                 395                 400

Val Ala Arg Leu Ala Glu Gln Arg Gly Asp Val Arg Ala Ala Gln Val
                405                 410                 415

Ala Leu Lys Asp Ala Val Lys Asn Asp Pro Asp Asn Val Trp Thr Arg
            420                 425                 430

Phe Asp Leu Ala Arg Leu Tyr Leu Lys Thr Asp Glu Ala Pro Lys Ala
        435                 440                 445

Arg Ala Leu Ile Asp Glu Leu Leu Lys Ala Gln Pro Asn Asn Ile Asp
    450                 455                 460

Ala Leu Tyr Thr Ser Ala Leu Leu Ser Val Glu Met Gly Gln Trp Gln
465                 470                 475                 480

Asp Ala Gln Thr Thr Phe Thr Arg Ile Pro Val Asp Gln Arg Thr Pro
                485                 490                 495

Asp Met Lys Ala Leu Ala Asp Glu Val Thr Met Thr Val Gln Ile Asn
            500                 505                 510

Leu Ala Ile Gly Ile Ala Arg Arg Gly Gln Arg Gln Glu Ala Leu Ala
        515                 520                 525

Leu Leu Asp Arg Leu Gln Pro Val Ala Ser Gly Ser Pro Glu Arg Gln
    530                 535                 540

Leu Thr Leu Ala Ser Ala Tyr Ile Asp Ala Gly Glu Pro Ala Arg Gly
545                 550                 555                 560

Arg Glu Met Ala Arg Ala Ala Ile Ala Gln Ala Pro Leu Pro Ser Ala
                565                 570                 575

Asp Leu Met Leu Gln Tyr Ala Gly Leu Leu Leu Ala Ala Gly Asp Asp
            580                 585                 590

Val Gln Val Asn Ala Ile Leu Arg Asn Val Gln Gly Gln Pro Met Ser
        595                 600                 605
```

-continued

```
Val Gln Thr Arg Lys Arg Phe Asp Asp Leu Leu Tyr Arg Tyr Arg Ile
    610                 615                 620

Arg Gln Ala Asp Leu Leu Arg Glu Gly Gly Asp Leu Ala Gly Ala Tyr
625                 630                 635                 640

Asp Thr Leu Ala Pro Ala Leu Ala Gln Arg Pro Asp Asp Ile Gln Ala
                645                 650                 655

Val Ser Ala Phe Ala Arg Met Tyr Thr Ala Asn Gly Asp Ser Ala Arg
            660                 665                 670

Ala Phe Glu Leu Tyr Lys Pro Leu Leu Gln Arg Gln Pro Asn Asp Pro
        675                 680                 685

Gln Val Leu Leu Gly Ala Ala Asp Ala Ala Val Lys Ala His Asp Tyr
    690                 695                 700

Gly Phe Ala Glu Lys Ala Leu Ser Gln Phe Arg Lys Leu Glu Arg Asn
705                 710                 715                 720

Asp Pro Gln Thr Leu Thr Glu Ala Ala Arg Ile Tyr Gln Ser Met Gly
                725                 730                 735

Gln Thr Gly Ala Ala Thr Glu Leu Leu Arg Lys Ala Val Ala Ile Glu
            740                 745                 750

Gln Ser Glu Lys Gln Arg Ala Met Ala Val Gln Ala Val Ser Thr Ser
        755                 760                 765

Thr Thr Ser Ser Asn Pro Phe Ala Thr Gly Gly Ser Arg Ser Leu Ala
    770                 775                 780

Ala Ala Ser Ala Ile Pro Ala Pro Ala Gln Val Ser Leu Ser Gly Gly
785                 790                 795                 800

Arg Ala Leu Glu Thr Asn Ser Ala Pro Glu Ile Ser Ala Pro Arg Asp
                805                 810                 815

Thr Ala Tyr Pro Gly Gln Ile Ala Ala Pro Gln Pro Leu Ser Ala Ala
            820                 825                 830

Arg Thr Gln Ser Val Arg Gly Asn Pro Phe Met Ala Ala Thr Asp Arg
        835                 840                 845

Asp Gln Ala Ser Ser Ala Gln Gln Ala Leu Asn Arg Ile Leu Glu Gln
    850                 855                 860

Arg Ser Gly Phe Val Ser Gln Gly Leu Ala Val Arg Ser Asn Asn Ser
865                 870                 875                 880

Glu Ser Gly Leu Ser Lys Leu Thr Val Val Glu Thr Pro Leu Glu Val
                885                 890                 895

Asn Leu Pro Ala Gly Asp Asn Arg Val Ala Val Arg Val Thr Pro Val
            900                 905                 910

Ser Leu Asn Ala Gly Ser Leu Lys Ser Asp Ala Gly Ala Arg Phe Gly
        915                 920                 925

Gly Gly Thr Ser Gly Ala Ala Gly Ser Gln Ser Asp Lys Gly Val Gly
    930                 935                 940

Leu Ala Val Ala Phe Glu Arg Pro Glu Glu Gly Leu Lys Ala Asp Ile
945                 950                 955                 960

Gly Thr Thr Pro Met Gly Phe Lys Tyr Thr Thr Val Ala Gly Gly Ala
                965                 970                 975

Ser Val Asp Arg Pro Leu Gly Asn Asn Pro Asp Leu Arg Tyr Gly Leu
            980                 985                 990

Asn Val Ser Arg Arg Pro Val Thr Asp Ser Val Thr Ser Phe Ala Gly
        995                1000                1005

Ser Thr Asp Glu Arg Ser Gly Leu Ser Trp Gly Gly Val Thr Ala Asn
   1010                1015                1020
```

-continued

```
Gly Gly Arg Gly Gln Leu Ser Tyr Asp Asp Gln Thr Ile Gly Gly Tyr
1025               1030                1035                1040

Gly Tyr Gly Ser Trp His Lys Leu Val Gly Asn Asn Val Lys Ser Asn
                1045                1050                1055

Thr Arg Gly Glu Val Gly Gly Gly Val Tyr Trp Tyr Leu Arg Asn Ala
            1060                1065                1070

Glu Asp Ser Lys Leu Thr Ala Gly Leu Ser Leu Met Gly Met Ser Tyr
        1075                1080                1085

Asp Asn Asp Gln Ser Tyr Phe Thr Tyr Gly His Gly Gly Tyr Phe Ser
    1090                1095                1100

Pro Gln Ser Phe Tyr Ala Ile Gly Val Pro Val Met Trp Ala Gln Arg
1105                1110                1115                1120

Thr Glu Arg Phe Ser Tyr Gln Val Lys Ser Ser Val Gly Val Gln His
                1125                1130                1135

Phe Lys Gln Asp Gly Ala Glu Phe Phe Pro Asp Asp Ser Thr Leu Gln
            1140                1145                1150

Ala Ala Ser Ala Gln Arg Tyr Thr Gly Gln Ser Lys Thr Gly Ile Gly
        1155                1160                1165

Tyr Asn Leu Ser Ala Ala Gly Glu Tyr Lys Leu Asp Ser Ser Leu Phe
    1170                1175                1180

Met Gly Ala Ser Leu Gly Leu Asp Asn Ala Arg Asp Tyr Arg Gln Phe
1185                1190                1195                1200

Ser Gly Ala Leu Tyr Leu Arg Tyr Met Phe Glu Asp Ile Thr Gly Pro
                1205                1210                1215

Met Ala Leu Pro Val Ser Pro Tyr Arg Ser Pro Tyr Ser Asn
            1220                1225                1230


<210> SEQ ID NO 73
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 73

atgaaactga tacgacagat ccgctcgcag ggtcgtcagt cgcccttgtt cgaggacctt     60

gcccagctcg aggggcgcaa gcgtcaatgg ctggccgagc gcgccgtgca gttcgcactg    120

ggcttgcacg gccgccggcc agaggtcgat aacccccttca aaggcaaact gcgtgaagac    180

ctgtgctgca tcatgttcga tgacctgtcg ctgcacaccc tggtcgagcg ttacgcggcc    240

agtgaagccc tgcgacgaca cgacagcgag tacttcagca aactgatcgc cacgacacga    300

aataccgtgg aacggcgcat cgtctttcac gggctgctgg aacacttcga caggctgttg    360

cctatcgaaa agagcatcta ccaactcaac taccgcagcg ttcaatacgc gcacctggag    420

caggaagaag ccctgtacgg caaactgata atggaacaac ccattagtgc actgctggaa    480

gtgcacacgc ctgagtggct tcttgagaat ctgtcttcgt ttgagttttc gattgattga    540


<210> SEQ ID NO 74
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 74

Met Lys Leu Ile Arg Gln Ile Arg Ser Gln Gly Arg Gln Ser Pro Leu
  1               5                  10                  15

Phe Glu Asp Leu Ala Gln Leu Glu Gly Arg Lys Arg Gln Trp Leu Ala
             20                  25                  30
```

-continued

```
Glu Arg Ala Val Gln Phe Ala Leu Gly Leu His Gly Arg Arg Pro Glu
         35                  40                  45

Val Asp Asn Pro Phe Lys Gly Lys Leu Arg Glu Asp Leu Cys Cys Ile
     50                  55                  60

Met Phe Asp Asp Leu Ser Leu His Thr Leu Val Glu Arg Tyr Ala Ala
 65                  70                  75                  80

Ser Glu Ala Leu Arg Arg His Asp Ser Glu Tyr Phe Ser Lys Leu Ile
                 85                  90                  95

Ala Thr Thr Arg Asn Thr Val Glu Arg Arg Ile Val Phe His Gly Leu
            100                 105                 110

Leu Glu His Phe Asp Arg Leu Leu Pro Ile Glu Lys Ser Ile Tyr Gln
        115                 120                 125

Leu Asn Tyr Arg Ser Val Gln Tyr Ala His Leu Glu Gln Glu Glu Ala
    130                 135                 140

Leu Tyr Gly Lys Leu Ile Met Glu Gln Pro Ile Ser Ala Leu Leu Glu
145                 150                 155                 160

Val His Thr Pro Glu Trp Leu Leu Glu Asn Leu Ser Ser Phe Glu Phe
                165                 170                 175
Ser Ile Asp
```

<210> SEQ ID NO 75
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 75

```
atgcgactga ctactaaagg ccgatacgct gtgacagcca tgcttgacct ggcgttacat     60

gcgcagaacg ggccagtgtc tctggccgac atctccgagc ggcagggcat ttccctgtct    120

tatctcgaac agttgttcgc caaactgcgt cgcggcaatc tggtttccag tgttcgtggt    180

ccgggcggcg gttatcagct gtctcgtgac atgaaaggca tccaggtcgc ccaagtcgtc    240

gacgcggtca atgaatcggt cgatgccacg cgttgtcagg ggctgggtga ttgccacgct    300

ggcgatacct gcctgaccca ccacttgtgg tgcgatctga gccagcagat tcacgaattt    360

ctaagcggta tcagcttggc ggatcttgtc actcgccgtg aggtacaaga agtcgctcag    420

cgccaggata tgcgccgtgg tcataaccac acgtcgcaac tgggtaagat cgaaacgtcc    480

gccgtcgaat ga                                                        492
```

<210> SEQ ID NO 76
<211> LENGTH: 163
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 76

```
Met Arg Leu Thr Thr Lys Gly Arg Tyr Ala Val Thr Ala Met Leu Asp
  1               5                  10                  15

Leu Ala Leu His Ala Gln Asn Gly Pro Val Ser Leu Ala Asp Ile Ser
             20                  25                  30

Glu Arg Gln Gly Ile Ser Leu Ser Tyr Leu Glu Gln Leu Phe Ala Lys
         35                  40                  45

Leu Arg Arg Gly Asn Leu Val Ser Ser Val Arg Gly Pro Gly Gly Gly
     50                  55                  60

Tyr Gln Leu Ser Arg Asp Met Lys Gly Ile Gln Val Ala Gln Val Val
 65                  70                  75                  80

Asp Ala Val Asn Glu Ser Val Asp Ala Thr Arg Cys Gln Gly Leu Gly
                 85                  90                  95
```

-continued

```
Asp Cys His Ala Gly Asp Thr Cys Leu Thr His His Leu Trp Cys Asp
            100                 105                 110

Leu Ser Gln Gln Ile His Glu Phe Leu Ser Gly Ile Ser Leu Ala Asp
        115                 120                 125

Leu Val Thr Arg Arg Glu Val Gln Glu Val Ala Gln Arg Gln Asp Met
    130                 135                 140

Arg Arg Gly His Asn His Thr Ser Gln Leu Gly Lys Ile Glu Thr Ser
145                 150                 155                 160
Ala Val Glu
```

<210> SEQ ID NO 77
<211> LENGTH: 3441
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 77

```
atgaataccg tcagaaaacc cataacacca cggatgctca gcatgaccga taaaaacggc     60

acccatcgac aacgacgtgc tgcactgttc cccaaaaccc cggcgaccgc caccagcctg    120

tgccctttca gagggcctaa tatcgccatc gtcccggtgc gctatgcgct ggatcgctcg    180

cgctatgacg ctgaccccgc gcaactgaag ccactgccca aagacggcca atgggcccac    240

ctgccgacgc tgaaaactcg cagttacacc ttacgccaac tgtacgacgg ctacgtttac    300

gtgttcgacg aaacggccgg cacgttgcac gaatacgcag cctcagccag cgacggccat    360

ctgagccgca tcgtctggac cgatgcacac atcggtaacg accagcgaag cggtgccggt    420

gaagggcaac cctttgtgct ttacccgcgt gaccaccgcc tgcacatcgc cttttctccc    480

ctgcaatgga catggcgaat gtgcgagcac atgcgctccc acgccccaag ccgcgcgttg    540

tggatgaagg cgctggacct ggccagctac tgcctcacca tggccgaacc ggacaccctg    600

ccgctggatc gcatcgccga ggccgtggcg gatatcgaca aagactgtgt tgtggaagat    660

ggccgttttg cagattcggc gattcccagt gttcgcccgc catcagaagg tgcagaaccc    720

tatccgttat gggcaccgct gggcgccgat gtcttctggc agggcagcgt ctacgatcag    780

gacagctctc tggtcattgc cctcaatgac ccgctcgccg ttttcaacga cttgggcatg    840

cagctggcgg ccgatcaggc ggcttttcgg gaatggcaaa gcgcccacga acacaagatc    900

cagattgccc agaccgtcgc cacgctgtgc ggtgcagaga gcgaagcaga gaagctgcca    960

gcatcggtgc gcggtgatgc gctgcgcacg catcagtacc tgagcgaggt cgaagcctac   1020

tttgaacaat gcattcttga agaagcacag atcagcagta gcaacgttcc tggagatttt   1080

ctgctgctgc cggacatgtt caagagcctg gacatgcgca aatcgatcga aacacgttat   1140

ggcagcgcgc cgaccgatga gggcgcgcag gcctggaaag atcgccacaa atggcggcgc   1200

gaggtcgatc tgagcagtgc gcgtcagtac cttttgcagc acctgccgac cggagacaaa   1260

cgcctgcaac aggtgcgtga cacgcaaagc gatttccagc actgggcggc acatataggc   1320

accgaaccgc tcaagctgtt catcgacacc acacacccga aaaccctgct gtatttgcag   1380

acgatcatgc tcaatctgca gatcatctat gcgcaggaca gcgccgcaaa tgcctggctc   1440

gccgagcagg aagccaacac cagcagcctg tttggcaccc tgcgttatgg tttttcgcca   1500

gcgctcaagc acgccctgca tcaggaagcc gacgcactgc tgaacggcct cggcgacgtc   1560

actaatctgg ccacgcgcat cggtgaactc aatggcgtgc tcaaccatca gggttttgcc   1620

gacaagccgt ggatgaaggc gctgaaacag cctgttcaag acaccttcaa agccctcggc   1680

gaactggcca gcggtgccgg caaagccagg tttgaaagtg tattactggc atgggtgccc   1740
```

-continued

atcgacagcc gcatggccct tggcaagcag cagaacatcg ttgcgttgct tcgcaccctg 1800

ctgatcggcc agatattgct cgactcgaca gcacgcgtcg cgatcaatga gcagacagtg 1860

accaagctca aacagtgggt aagtgagtgg caagtcctca acaagcaaat cagcgagctg 1920

gtgcgcagtt ggcaataccc gaacgcctac aacacgcgcc aaagcaccgc tcgcaaattg 1980

caggcccata aacacaaact gcgcgttcac gaactgagca tccctgccct gctcgacttt 2040

cagaacaacg aatacgccaa gctattgcag gacgagattc gtcagtactt ccagtctggc 2100

aaaaccctcg ccacggactg gctcgcccgc gccaaaggct ggaccgaccg actgggcggc 2160

gttgctggca cgatcacctg gggcgtggtc atgcttaacc tgatcaatac cgccttcctc 2220

tatcgggacc ttacccggga cggggatttc agtaccaagg acattggcaa ggtgacgtat 2280

ggattggggt acagcttcaa tctgttgatg gcggtgtttg tggacgcgcc gtggagcatc 2340

ataagggacg caacgccagc gctgatcgat ggcaagaatg tggccattct ggacaggtcc 2400

agtgcgtact ggaaagccaa gggaaatgca gcgtggggtg atgcgatacg tgggttcagg 2460

gtttcgatgg tggcgatggg tgggtttggg cttgcggcgg ttacgcttga attatttgat 2520

gttacagatg attttcacgc agctaaaaca tcagaagaaa catatggaat tggcatcaag 2580

gggttttccg tagtggtgat gggattgggt gctgcggccc agctaatggc aggcatttct 2640

cccgctggcg tttttacgat tatcgcaatg agtccgtggt tcagcgtagc gctactggca 2700

gcaggcttga tttatctttt tgctacgatg gcccttaatt acttcaagca agacagtgtc 2760

ggctggtggc tacgcaagtg ctgttggtcc ataacccaag actatcgcta tgctgagact 2820

gcggaaggta agcatgacga agtgcgcgcg ctgatggaaa taaaattatc tccgcaggtc 2880

catgtaaaaa gcaccgtgaa ttatgaaaac cgttatcttg gcaaaaacga tcactacagc 2940

gtagcggtac aaaatggcgc gggggtacaa gtgcgcttgc cgaatcttct acgcgggctg 3000

tccgtgcatt tcaatatcgt tagtagcaag agaccatggg gcgtgctgcc cgtagaaaaa 3060

atagatcagc cgatacatga agcttttctg gaccacgggc aattcaggaa agtcgaacag 3120

ttcgggatgt ttaccaacaa gcctgctggc aaggcgagtg aagactatac ctacccccgc 3180

atgccacctg aaaacgaaga cctcatctgg gaaacctggg tgccgctcga caaggacgca 3240

acgtatcttg agttgcaaat ctggtacccg gccaatcttt taaatcctgg cggagacgat 3300

agaagctatc tgtttcagat ggagcttggc acaaaaggcg ataccgctat tgacggcctg 3360

gctgcagtgg aactcgaggt aaaggcatca agcaggattg gcgctctgac cctagaagtc 3420

gcagagggca cacctgtatg a 3441

<210> SEQ ID NO 78
<211> LENGTH: 1146
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 78

Met Asn Thr Val Arg Lys Pro Ile Thr Pro Arg Met Leu Ser Met Thr
1 5 10 15

Asp Lys Asn Gly Thr His Arg Gln Arg Arg Ala Ala Leu Phe Pro Lys
20 25 30

Thr Pro Ala Thr Ala Thr Ser Leu Cys Pro Phe Arg Gly Pro Asn Ile
35 40 45

Ala Ile Val Pro Val Arg Tyr Ala Leu Asp Arg Ser Arg Tyr Asp Ala
50 55 60

-continued

```
Asp Pro Ala Gln Leu Lys Pro Leu Pro Lys Asp Gly Gln Trp Ala His
 65                  70                  75                  80

Leu Pro Thr Leu Lys Thr Arg Ser Tyr Thr Leu Arg Gln Leu Tyr Asp
                85                  90                  95

Gly Tyr Val Tyr Val Phe Asp Glu Thr Ala Gly Thr Leu His Glu Tyr
            100                 105                 110

Ala Ala Ser Ala Ser Asp Gly His Leu Ser Arg Ile Val Trp Thr Asp
        115                 120                 125

Ala His Ile Gly Asn Asp Gln Arg Ser Gly Ala Gly Glu Gly Gln Pro
    130                 135                 140

Phe Val Leu Tyr Pro Arg Asp His Arg Leu His Ile Ala Phe Ser Pro
145                 150                 155                 160

Leu Gln Trp Thr Trp Arg Met Cys Glu His Met Arg Ser His Ala Pro
                165                 170                 175

Ser Arg Ala Leu Trp Met Lys Ala Leu Asp Leu Ala Ser Tyr Cys Leu
            180                 185                 190

Thr Met Ala Glu Pro Asp Thr Leu Pro Leu Asp Arg Ile Ala Glu Ala
        195                 200                 205

Val Ala Asp Ile Asp Lys Asp Cys Val Val Glu Asp Gly Arg Phe Ala
    210                 215                 220

Asp Ser Ala Ile Pro Ser Val Arg Pro Pro Ser Glu Gly Ala Glu Pro
225                 230                 235                 240

Tyr Pro Leu Trp Ala Pro Leu Gly Ala Asp Val Phe Trp Gln Gly Ser
                245                 250                 255

Val Tyr Asp Gln Asp Ser Ser Leu Val Ile Ala Leu Asn Asp Pro Leu
            260                 265                 270

Ala Val Phe Asn Asp Leu Gly Met Gln Leu Ala Ala Asp Gln Ala Ala
        275                 280                 285

Phe Arg Glu Trp Gln Ser Ala His Glu His Lys Ile Gln Ile Ala Gln
    290                 295                 300

Thr Val Ala Thr Leu Cys Gly Ala Glu Ser Glu Ala Glu Lys Leu Pro
305                 310                 315                 320

Ala Ser Val Arg Gly Asp Ala Leu Arg Thr His Gln Tyr Leu Ser Glu
                325                 330                 335

Val Glu Ala Tyr Phe Glu Gln Cys Ile Leu Glu Glu Ala Gln Ile Ser
            340                 345                 350

Ser Ser Asn Val Pro Gly Asp Phe Leu Leu Leu Pro Asp Met Phe Lys
        355                 360                 365

Ser Leu Asp Met Arg Lys Ser Ile Glu Thr Arg Tyr Gly Ser Ala Pro
    370                 375                 380

Thr Asp Glu Gly Ala Gln Ala Trp Lys Asp Arg His Lys Trp Arg Arg
385                 390                 395                 400

Glu Val Asp Leu Ser Ser Ala Arg Gln Tyr Leu Leu Gln His Leu Pro
                405                 410                 415

Thr Gly Asp Lys Arg Leu Gln Gln Val Arg Asp Thr Gln Ser Asp Phe
            420                 425                 430

Gln His Trp Ala Ala His Ile Gly Thr Glu Pro Leu Lys Leu Phe Ile
        435                 440                 445

Asp Thr Thr His Pro Lys Thr Leu Leu Tyr Leu Gln Thr Ile Met Leu
    450                 455                 460

Asn Leu Gln Ile Ile Tyr Ala Gln Asp Ser Ala Ala Asn Ala Trp Leu
465                 470                 475                 480
```

-continued

```
Ala Glu Gln Glu Ala Asn Thr Ser Ser Leu Phe Gly Thr Leu Arg Tyr
                485                 490                 495

Gly Phe Ser Pro Ala Leu Lys His Ala Leu His Gln Glu Ala Asp Ala
            500                 505                 510

Leu Leu Asn Gly Leu Gly Asp Val Thr Asn Leu Ala Thr Arg Ile Gly
        515                 520                 525

Glu Leu Asn Gly Val Leu Asn His Gln Gly Phe Ala Asp Lys Pro Trp
    530                 535                 540

Met Lys Ala Leu Lys Gln Pro Val Gln Asp Thr Phe Lys Ala Leu Gly
545                 550                 555                 560

Glu Leu Ala Ser Gly Ala Gly Lys Ala Arg Phe Glu Ser Val Leu Leu
                565                 570                 575

Ala Trp Val Pro Ile Asp Ser Arg Met Ala Leu Gly Lys Gln Gln Asn
            580                 585                 590

Ile Val Ala Leu Leu Arg Thr Leu Leu Ile Gly Gln Ile Leu Leu Asp
        595                 600                 605

Ser Thr Ala Arg Val Ala Ile Asn Glu Gln Thr Val Thr Lys Leu Lys
    610                 615                 620

Gln Trp Val Ser Glu Trp Gln Val Leu Asn Lys Gln Ile Ser Glu Leu
625                 630                 635                 640

Val Arg Ser Trp Gln Tyr Pro Asn Ala Tyr Asn Thr Arg Gln Ser Thr
                645                 650                 655

Ala Arg Lys Leu Gln Ala His Lys His Lys Leu Arg Val His Glu Leu
            660                 665                 670

Ser Ile Pro Ala Leu Leu Asp Phe Gln Asn Asn Glu Tyr Ala Lys Leu
        675                 680                 685

Leu Gln Asp Glu Ile Arg Gln Tyr Phe Gln Ser Gly Lys Thr Leu Ala
    690                 695                 700

Thr Asp Trp Leu Ala Arg Ala Lys Gly Trp Thr Asp Arg Leu Gly Gly
705                 710                 715                 720

Val Ala Gly Thr Ile Thr Trp Gly Val Val Met Leu Asn Leu Ile Asn
                725                 730                 735

Thr Ala Phe Leu Tyr Arg Asp Leu Thr Arg Asp Gly Asp Phe Ser Thr
            740                 745                 750

Lys Asp Ile Gly Lys Val Thr Tyr Gly Leu Gly Tyr Ser Phe Asn Leu
        755                 760                 765

Leu Met Ala Val Phe Val Asp Ala Pro Trp Ser Ile Ile Arg Asp Ala
    770                 775                 780

Thr Pro Ala Leu Ile Asp Gly Lys Asn Val Ala Ile Leu Asp Arg Ser
785                 790                 795                 800

Ser Ala Tyr Trp Lys Ala Lys Gly Asn Ala Ala Trp Gly Asp Ala Ile
                805                 810                 815

Arg Gly Phe Arg Val Ser Met Val Ala Met Gly Gly Phe Gly Leu Ala
            820                 825                 830

Ala Val Thr Leu Glu Leu Phe Asp Val Thr Asp Asp Phe His Ala Ala
        835                 840                 845

Lys Thr Ser Glu Glu Thr Tyr Gly Ile Gly Ile Lys Gly Phe Ser Val
    850                 855                 860

Val Val Met Gly Leu Gly Ala Ala Ala Gln Leu Met Ala Gly Ile Ser
865                 870                 875                 880

Pro Ala Gly Val Phe Thr Ile Ile Ala Met Ser Pro Trp Phe Ser Val
                885                 890                 895
```

-continued

```
Ala Leu Leu Ala Ala Gly Leu Ile Tyr Leu Phe Ala Thr Met Ala Leu
            900                 905                 910

Asn Tyr Phe Lys Gln Asp Ser Val Gly Trp Trp Leu Arg Lys Cys Cys
        915                 920                 925

Trp Ser Ile Thr Gln Asp Tyr Arg Tyr Ala Glu Thr Ala Glu Gly Lys
    930                 935                 940

His Asp Glu Val Arg Ala Leu Met Glu Ile Lys Leu Ser Pro Gln Val
945                 950                 955                 960

His Val Lys Ser Thr Val Asn Tyr Glu Asn Arg Tyr Leu Gly Lys Asn
                965                 970                 975

Asp His Tyr Ser Val Ala Val Gln Asn Gly Ala Gly Val Gln Val Arg
            980                 985                 990

Leu Pro Asn Leu Leu Arg Gly Leu Ser Val His Phe Asn Ile Val Ser
        995                1000                1005

Ser Lys Arg Pro Trp Gly Val Leu Pro Val Glu Lys Ile Asp Gln Pro
   1010                1015                1020

Ile His Glu Ala Phe Leu Asp His Gly Gln Phe Arg Lys Val Glu Gln
1025                1030                1035                1040

Phe Gly Met Phe Thr Asn Lys Pro Ala Gly Lys Ala Ser Glu Asp Tyr
               1045                1050                1055

Thr Tyr Pro Arg Met Pro Pro Glu Asn Glu Asp Leu Ile Trp Glu Thr
           1060                1065                1070

Trp Val Pro Leu Asp Lys Asp Ala Thr Tyr Leu Glu Leu Gln Ile Trp
       1075                1080                1085

Tyr Pro Ala Asn Leu Leu Asn Pro Gly Gly Asp Asp Arg Ser Tyr Leu
   1090                1095                1100

Phe Gln Met Glu Leu Gly Thr Lys Gly Asp Thr Ala Ile Asp Gly Leu
1105                1110                1115                1120

Ala Ala Val Glu Leu Glu Val Lys Ala Ser Ser Arg Ile Gly Ala Leu
               1125                1130                1135

Thr Leu Glu Val Ala Glu Gly Thr Pro Val
           1140                1145
```

<210> SEQ ID NO 79
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 79

```
atgtgcctgg tggcgagcct gtcggtgctg gcaggcatga ccgatgccat cggcttcatg     60

gccaccggcg atttcgtctc gttcatgagc ggcaacacca cgcgccttgc ggtggcgatc    120

agtgatggcg atttgagcgt cacactccgt ctggccctgg ccatctttgc gtttattgcc    180

ggcaatgcac tgggcgttgt cgttgcgcgc ctgggcaacc ggcgcgccct gcccttactg    240

ctggctatcg ccacgctgtt gtgtgccgct gcggcgtggc cgttggcgaa caatatgctt    300

gccctgatct gggcgattct ggcgatgggc atgctcaacg ccgctgtcga gcaggtcaac    360

gggctgccgg tgggcctgac ctacgtgacc ggcgcgctgt cgcgactggg gcgcggtctg    420

ggccgctgga tgctcggcga acgccgggat ggctggcgca ttcaactggt cccgtgggcc    480

gggatgttca ttggcgcagt gatcggcgcg ttgcttgaac atcgtctggg gctcaatgcc    540

ttgctggtca gcgccagcct gtcagcgtta atggcgctgg tgtcgctgaa aatcccgcat    600

cgctggcaac gtcagtacat gccgcgctga                                     630
```

-continued

<210> SEQ ID NO 80
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 80

Met Cys Leu Val Ala Ser Leu Ser Val Leu Ala Gly Met Thr Asp Ala
1 5 10 15

Ile Gly Phe Met Ala Thr Gly Asp Phe Val Ser Phe Met Ser Gly Asn
20 25 30

Thr Thr Arg Leu Ala Val Ala Ile Ser Asp Gly Asp Leu Ser Val Thr
35 40 45

Leu Arg Leu Ala Leu Ala Ile Phe Ala Phe Ile Ala Gly Asn Ala Leu
50 55 60

Gly Val Val Val Ala Arg Leu Gly Asn Arg Arg Ala Leu Pro Leu Leu
65 70 75 80

Leu Ala Ile Ala Thr Leu Leu Cys Ala Ala Ala Ala Trp Pro Leu Ala
85 90 95

Asn Asn Met Leu Ala Leu Ile Trp Ala Ile Leu Ala Met Gly Met Leu
100 105 110

Asn Ala Ala Val Glu Gln Val Asn Gly Leu Pro Val Gly Leu Thr Tyr
115 120 125

Val Thr Gly Ala Leu Ser Arg Leu Gly Arg Gly Leu Gly Arg Trp Met
130 135 140

Leu Gly Glu Arg Arg Asp Gly Trp Arg Ile Gln Leu Val Pro Trp Ala
145 150 155 160

Gly Met Phe Ile Gly Ala Val Ile Gly Ala Leu Leu Glu His Arg Leu
165 170 175

Gly Leu Asn Ala Leu Leu Val Ser Ala Ser Leu Ser Ala Leu Met Ala
180 185 190

Leu Val Ser Leu Lys Ile Pro His Arg Trp Gln Arg Gln Tyr Met Pro
195 200 205

Arg

<210> SEQ ID NO 81
<211> LENGTH: 882
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 81

atgagagggc ttggtgttct gagcatgaac caccagtttc agggcaatac cctgttcaaa 60

gaaataagcg gtaccagctt ttccgcgccc tacatcaccc atcttgcggg ccgtctcctt 120

aacgagcacc cagaggcatc ggcgaacctc ttgcgcgcta tgctggtgaa tcatgcgtca 180

ttgtctagcg aggtcgagac gactttctcc gacgacatga ggaagggcta caaagctaat 240

aaggcgaccc acaaccgtga aatatcgcgc gatgtgagtg gttacggcca agtgaatgag 300

gcagacctgt ttcggtcttc cgaccattgc gttgtgctga tgtgtgaaga gtccattgag 360

aaggactcgt gccagttcta cgaactgcct ttgcccactt cgtttcttcg cagggctaga 420

ggggcaaggc acctgagcgt cacgctggct tattctcctg ccgtcaggac aactcggttg 480

gactatctgg caactcagat cagttatcgc ctagtgaaag gttcgtcgct tgaggaagtc 540

caggcctcgt ttaactacga caagcaggac gaaacgaaga cccgtggaga tgacgctgag 600

cagaatcgag acatcactgc tcagttgaga agccgcggga ccgtccagtc ctcgcggtgg 660

acgttcaaga agcgaaatcc agaagaaaaa tggtttgtag ttgtgatccg ccaggatcgg 720

-continued

gaatggaatc atcccgacgt gctggatcga gaatcttacg ccctggtggt aacagttgct 780

gatcgtgaca acgaacacgc gcagttgtat gccgaaattc aagccaagct gacgcttcaa 840

aatcaggtgc gtgaagaggc aaggcagcgg gctgttctgt aa 882

<210> SEQ ID NO 82
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 82

Met Arg Gly Leu Gly Val Leu Ser Met Asn His Gln Phe Gln Gly Asn
1 5 10 15

Thr Leu Phe Lys Glu Ile Ser Gly Thr Ser Phe Ser Ala Pro Tyr Ile
20 25 30

Thr His Leu Ala Gly Arg Leu Leu Asn Glu His Pro Glu Ala Ser Ala
35 40 45

Asn Leu Leu Arg Ala Met Leu Val Asn His Ala Ser Leu Ser Ser Glu
50 55 60

Val Glu Thr Thr Phe Ser Asp Asp Met Arg Lys Gly Tyr Lys Ala Asn
65 70 75 80

Lys Ala Thr His Asn Arg Glu Ile Ser Arg Asp Val Ser Gly Tyr Gly
85 90 95

Gln Val Asn Glu Ala Asp Leu Phe Arg Ser Ser Asp His Cys Val Val
100 105 110

Leu Met Cys Glu Glu Ser Ile Glu Lys Asp Ser Cys Gln Phe Tyr Glu
115 120 125

Leu Pro Leu Pro Thr Ser Phe Leu Arg Arg Ala Arg Gly Ala Arg His
130 135 140

Leu Ser Val Thr Leu Ala Tyr Ser Pro Ala Val Arg Thr Thr Arg Leu
145 150 155 160

Asp Tyr Leu Ala Thr Gln Ile Ser Tyr Arg Leu Val Lys Gly Ser Ser
165 170 175

Leu Glu Glu Val Gln Ala Ser Phe Asn Tyr Asp Lys Gln Asp Glu Thr
180 185 190

Lys Thr Arg Gly Asp Asp Ala Glu Gln Asn Arg Asp Ile Thr Ala Gln
195 200 205

Leu Arg Ser Arg Gly Thr Val Gln Ser Ser Arg Trp Thr Phe Lys Lys
210 215 220

Arg Asn Pro Glu Glu Lys Trp Phe Val Val Val Ile Arg Gln Asp Arg
225 230 235 240

Glu Trp Asn His Pro Asp Val Leu Asp Arg Glu Ser Tyr Ala Leu Val
245 250 255

Val Thr Val Ala Asp Arg Asp Asn Glu His Ala Gln Leu Tyr Ala Glu
260 265 270

Ile Gln Ala Lys Leu Thr Leu Gln Asn Gln Val Arg Glu Glu Ala Arg
275 280 285

Gln Arg Ala Val Leu
290

<210> SEQ ID NO 83
<211> LENGTH: 846
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 83

atgggcattg gcggtttgct taaacctttg gtcgattttt taccgaagtt gccgacctta 60

cgcaccaaga tttcctcgcc ttccatcagc tacgcgcgtt tgcaaagcga tgcgtcccag 120

gtacgcagta aattgggatt gggtgagcgc agcgtgctgg gttatgaagc gctgatcgcc 180

gagttcaagg cgtgcggggc ggttctggtg cccgttcttt ggggacaaaa gcagcaacac 240

aagaatgcgt tgcacattct attgccggcg tcagatgtca cctttgtctt cgtcaacctg 300

gataccaagc tggaagactt caagttttgg atggcccacg agttagcgca tgtctacact 360

cctgagcttg cgggtagtga cgagggggag gattttgcgg atgcctttgc cggtgccctg 420

ctgtttcctg aggcttgcgt gcagctagcg tatgccgagg cggcgcaagc gcctagcgca 480

gctggggagg tgagtgtcct tcagcagcat gcccggcatc accaaatttc actgaacacg 540

gtgttccagc aggcgcaggg atatgcggcg gaaaacaatc tgccatcctt acgggtaccg 600

gaaaggacaa ttcacgcggt gcgcaacagc tccacgccgc agttggtcag tacgatcctg 660

tttgatccga ctccacccaa accggcgcaa tacattgccg cagcgtcgaa tgtgtttcag 720

tctgagttct tcctggcgct gaaacgcatg attcgcgagc acgggacggg cccgtcgtat 780

gttcagcaaa tcatggatgt atcactcagt gatgcctccg cgctttacgg cgagctcgcg 840

cgttga 846

<210> SEQ ID NO 84
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 84

Met Gly Ile Gly Gly Leu Leu Lys Pro Leu Val Asp Phe Leu Pro Lys
1 5 10 15

Leu Pro Thr Leu Arg Thr Lys Ile Ser Ser Pro Ser Ile Ser Tyr Ala
20 25 30

Arg Leu Gln Ser Asp Ala Ser Gln Val Arg Ser Lys Leu Gly Leu Gly
35 40 45

Glu Arg Ser Val Leu Gly Tyr Glu Ala Leu Ile Ala Glu Phe Lys Ala
50 55 60

Cys Gly Ala Val Leu Val Pro Val Leu Trp Gly Gln Lys Gln Gln His
65 70 75 80

Lys Asn Ala Leu His Ile Leu Leu Pro Ala Ser Asp Val Thr Phe Val
85 90 95

Phe Val Asn Leu Asp Thr Lys Leu Glu Asp Phe Lys Phe Trp Met Ala
100 105 110

His Glu Leu Ala His Val Tyr Thr Pro Glu Leu Ala Gly Ser Asp Glu
115 120 125

Gly Glu Asp Phe Ala Asp Ala Phe Ala Gly Ala Leu Leu Phe Pro Glu
130 135 140

Ala Cys Val Gln Leu Ala Tyr Ala Glu Ala Ala Gln Ala Pro Ser Ala
145 150 155 160

Ala Gly Glu Val Ser Val Leu Gln Gln His Ala Arg His His Gln Ile
165 170 175

Ser Leu Asn Thr Val Phe Gln Gln Ala Gln Gly Tyr Ala Ala Glu Asn
180 185 190

Asn Leu Pro Ser Leu Arg Val Pro Glu Arg Thr Ile His Ala Val Arg
195 200 205

-continued

```
Asn Ser Ser Thr Pro Gln Leu Val Ser Thr Ile Leu Phe Asp Pro Thr
    210                 215                 220

Pro Pro Lys Pro Ala Gln Tyr Ile Ala Ala Ala Ser Asn Val Phe Gln
225                 230                 235                 240

Ser Glu Phe Phe Leu Ala Leu Lys Arg Met Ile Arg Glu His Gly Thr
                245                 250                 255

Gly Pro Ser Tyr Val Gln Gln Ile Met Asp Val Ser Leu Ser Asp Ala
            260                 265                 270

Ser Ala Leu Tyr Gly Glu Leu Ala Arg
        275                 280


<210> SEQ ID NO 85
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 85

atgaagcagc tcgcggcagg cagcaatgtg catgttcttg aaaatgagtc tttccagata     60

gataaggtgc gctttttggg ggccacagct tggacagatt tcgcaacagg tgaaagcgtg    120

taccaagcgt cccaggaggc aaggcgaggc atgaatgact ttcgcttgat ccgtgcaggc    180

gagggttacc gcgcattgag catcagtgat gtgatcagtc gaaatcatcg aacttacgag    240

tggctcaagg aagagctcgc catggagttc gatggtcaga ccattgtcat cactcatcat    300

tgcccgttgg tcaattactg tggcccagag cagggctcac cgctaatgcc tgcttattca    360

aatgattggc cagaactcgt tcgtcaggct gatgtgtggg tctttgggca cacgcacagt    420

catgtcgatg tcatggtgga aggatgccga ctcattagta accctagagg ttatccaggt    480

gagagttgcg gctttgccaa tgactttgtg gtcgatatta actag                    525


<210> SEQ ID NO 86
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 86

Met Lys Gln Leu Ala Ala Gly Ser Asn Val His Val Leu Glu Asn Glu
  1               5                  10                  15

Ser Phe Gln Ile Asp Lys Val Arg Phe Leu Gly Ala Thr Ala Trp Thr
             20                  25                  30

Asp Phe Ala Thr Gly Glu Ser Val Tyr Gln Ala Ser Gln Glu Ala Arg
         35                  40                  45

Arg Gly Met Asn Asp Phe Arg Leu Ile Arg Ala Gly Glu Gly Tyr Arg
     50                  55                  60

Ala Leu Ser Ile Ser Asp Val Ile Ser Arg Asn His Arg Thr Tyr Glu
 65                  70                  75                  80

Trp Leu Lys Glu Glu Leu Ala Met Glu Phe Asp Gly Gln Thr Ile Val
                 85                  90                  95

Ile Thr His His Cys Pro Leu Val Asn Tyr Cys Gly Pro Glu Gln Gly
            100                 105                 110

Ser Pro Leu Met Pro Ala Tyr Ser Asn Asp Trp Pro Glu Leu Val Arg
        115                 120                 125

Gln Ala Asp Val Trp Val Phe Gly His Thr His Ser His Val Asp Val
    130                 135                 140
```

-continued

Met Val Glu Gly Cys Arg Leu Ile Ser Asn Pro Arg Gly Tyr Pro Gly
145 150 155 160

Glu Ser Cys Gly Phe Ala Asn Asp Phe Val Val Asp Ile Asn
165 170

<210> SEQ ID NO 87
<211> LENGTH: 2307
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 87

atgacgctga cgcagcgtca ggcatggcat cgcgaggcac agcggtttgg cgagcaggtg 60

gtgaacatgc gcaaagccag caaggagcac ttcggccagg cggaaaatga cagccgcacc 120

tatccggcgc gctttatcga ccagcaactg gctcaactgc tgaaccggct atccatcgct 180

gcaacggcgc aacagatcaa tatttcactg acctacagga cgggcaccga agtgctcgaa 240

attcccggcg cgcctgtatt gccagaaacc gagaccgaga acgtttcact caggcaactg 300

gtgcataccc aggccctgcg caccaaggcc aaggatgccg tgcttctacg cgctgtcgac 360

gccgaaggcg tccccccttgc gcacttggac aagcaggccg taaccgagct gattgccacg 420

ctggaagatc accgatacct cagtgattac cttgacctgc acctgaaaac ctcggcgtat 480

gcacagcagc tcaagcggtc agaaaaagcc atgttgcaag ctcagatgaa gatggcgctg 540

ctggagatcg agcaacaggc ttttgcacca gccggtcgcg agtggatcaa ggctgtgctg 600

gattcgccag ccccccaagg acgtcgaacc atggcagggg aaagcattga agtccgtttt 660

ttcagcgtca accaattcaa gatgaccaat gtcatgctga ttgctccagc cggtaaattc 720

gagaaggggc cgctggtgct ttgcacgctg gatgcttccg acggtgtggt tttccgctgg 780

tttaacagca tgtatcacct gaccaccagc tttctggaag aggcaccctt ccagcagtat 840

ctgattcagc aaataccggt ttccaggcgt cttgagacgc tgcatgccat gcagtacgaa 900

aaggaagcca agcattggcg tccgccagaa gtattcaccc aactgacgct gctaccgatc 960

ccgtcaaggc tgctgcgccc agtcgtgttt gtcagccaga gcaaagacat ttacgaggaa 1020

aatcacgaga ccaagatcaa ccatctgatc aacgaagcca aacggcagat gagcctgtcc 1080

accggtacag ggcaatcggg tcggggcttc gatctgatcg cgagcattgc gattctgttt 1140

ctgcctggcg cgatcatgat gcctgtctcg ctgggcgctg gcctttacaa aacctggagc 1200

gctttttcga aaatcgatga aaacgacctg gaaggtgccg ccgaggagtt tctgagcgcc 1260

ctcagctatc ttgccattac cttggtcggc catttggcgc tggccttgaa accggcagga 1320

agcgccgcaa aaacggtgag acgtccgcac ctggtacgca gagtcggtcg tgatgggcag 1380

gcacagatcg gctacctcct gtcgcattca aaagcgccgc gtttcccaga ctcgaaattg 1440

atcgctgcaa tggaccccaa acgcttcgtc gccattgagg tagaaggcca gacctgctta 1500

ataagccggc gggccaacct gttcggccac tcacgccttt atcgggtaaa cccgatggat 1560

gcaacgcaac tggtgcacga gcaggagttt gccttgcgca gcaccaacgg cacctggaaa 1620

atcgtgggca aacagatcct gcgcatgagt cagtccgcaa tccgcaatgc ccaggctcaa 1680

ctgaccagcc tgacaaatct ctggccggcg tctctggagg aagcaagtag cgccgaacgc 1740

ttgagcttcg agaccgacta cctggcgctg gcccagacat ccaacgcaga aaactattcc 1800

gaaatagtcg cctacgtgga aagcggttca acagacatca acccgctgct gcgaagcggc 1860

gtgcgcaacg ccaccacgcg cagattttta cgtcagttcc ataaactcaa tgcgtgggaa 1920

ggcactgcct ttcgcgccac ctatgtgtcc agcgacgggg tggcatgcct tgagcgcgaa 1980

-continued

```
gtgggttcgg tgttcaccga caacggcgtg cagtctgcat cggtgtcgcg agccaatgcc   2040

tccagatgga gccaggacgg gttcgtgagc agcaacgcca atgccgcaaa ccacccggtg   2100

ttcttcatct ttgcaccggg agtgcccaag aagaacatgt tcaccggctt tcttggcgat   2160

cacgtggcaa tcccgccagg cacgtgcgtg caactgggtg cgaccaagcg gataaacgga   2220

cagctgtttg cctggttcga tgcgcccgaa caaatggtcg atcagaccta cgatctctat   2280

acaggagaac aggaactctg ggtctga                                       2307
```

<210> SEQ ID NO 88
<211> LENGTH: 768
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 88

```
Met Thr Leu Thr Gln Arg Gln Ala Trp His Arg Glu Ala Gln Arg Phe
  1               5                  10                  15

Gly Glu Gln Val Val Asn Met Arg Lys Ala Ser Lys Glu His Phe Gly
             20                  25                  30

Gln Ala Glu Asn Asp Ser Arg Thr Tyr Pro Ala Arg Phe Ile Asp Gln
         35                  40                  45

Gln Leu Ala Gln Leu Leu Asn Arg Leu Ser Ile Ala Ala Thr Ala Gln
     50                  55                  60

Gln Ile Asn Ile Ser Leu Thr Tyr Arg Thr Gly Thr Glu Val Leu Glu
 65                  70                  75                  80

Ile Pro Gly Ala Pro Val Leu Pro Glu Thr Glu Thr Glu Asn Val Ser
                 85                  90                  95

Leu Arg Gln Leu Val His Thr Gln Ala Leu Arg Thr Lys Ala Lys Asp
            100                 105                 110

Ala Val Leu Leu Arg Ala Val Asp Ala Glu Gly Val Pro Leu Ala His
        115                 120                 125

Leu Asp Lys Gln Ala Val Thr Glu Leu Ile Ala Thr Leu Glu Asp His
    130                 135                 140

Arg Tyr Leu Ser Asp Tyr Leu Asp Leu His Leu Lys Thr Ser Ala Tyr
145                 150                 155                 160

Ala Gln Gln Leu Lys Arg Ser Glu Lys Ala Met Leu Gln Ala Gln Met
                165                 170                 175

Lys Met Ala Leu Leu Glu Ile Glu Gln Gln Ala Phe Ala Pro Ala Gly
            180                 185                 190

Arg Glu Trp Ile Lys Ala Val Leu Asp Ser Pro Ala Pro Gln Gly Arg
        195                 200                 205

Arg Thr Met Ala Gly Glu Ser Ile Glu Val Arg Phe Phe Ser Val Asn
    210                 215                 220

Gln Phe Lys Met Thr Asn Val Met Leu Ile Ala Pro Ala Gly Lys Phe
225                 230                 235                 240

Glu Lys Gly Pro Leu Val Leu Cys Thr Leu Asp Ala Ser Asp Gly Val
                245                 250                 255

Val Phe Arg Trp Phe Asn Ser Met Tyr His Leu Thr Thr Ser Phe Leu
            260                 265                 270

Glu Glu Ala Pro Phe Gln Gln Tyr Leu Ile Gln Gln Ile Pro Val Ser
        275                 280                 285

Arg Arg Leu Glu Thr Leu His Ala Met Gln Tyr Glu Lys Glu Ala Lys
    290                 295                 300

His Trp Arg Pro Pro Glu Val Phe Thr Gln Leu Thr Leu Leu Pro Ile
305                 310                 315                 320
```

-continued

```
Pro Ser Arg Leu Leu Arg Pro Val Val Phe Val Ser Gln Ser Lys Asp
                325                 330                 335

Ile Tyr Glu Glu Asn His Glu Thr Lys Ile Asn His Leu Ile Asn Glu
            340                 345                 350

Ala Lys Arg Gln Met Ser Leu Ser Thr Gly Thr Gly Gln Ser Gly Arg
        355                 360                 365

Gly Phe Asp Leu Ile Ala Ser Ile Ala Ile Leu Phe Leu Pro Gly Ala
    370                 375                 380

Ile Met Met Pro Val Ser Leu Gly Ala Gly Leu Tyr Lys Thr Trp Ser
385                 390                 395                 400

Ala Phe Ser Lys Ile Asp Glu Asn Asp Leu Glu Gly Ala Ala Glu Glu
                405                 410                 415

Phe Leu Ser Ala Leu Ser Tyr Leu Ala Ile Thr Leu Val Gly His Leu
            420                 425                 430

Ala Leu Ala Leu Lys Pro Ala Gly Ser Ala Ala Lys Thr Val Arg Arg
        435                 440                 445

Pro His Leu Val Arg Arg Val Gly Arg Asp Gly Gln Ala Gln Ile Gly
    450                 455                 460

Tyr Leu Leu Ser His Ser Lys Ala Pro Arg Phe Pro Asp Ser Lys Leu
465                 470                 475                 480

Ile Ala Ala Met Asp Pro Lys Arg Phe Val Ala Ile Glu Val Glu Gly
                485                 490                 495

Gln Thr Cys Leu Ile Ser Arg Arg Ala Asn Leu Phe Gly His Ser Arg
            500                 505                 510

Leu Tyr Arg Val Asn Pro Met Asp Ala Thr Gln Leu Val His Glu Gln
        515                 520                 525

Glu Phe Ala Leu Arg Ser Thr Asn Gly Thr Trp Lys Ile Val Gly Lys
    530                 535                 540

Gln Ile Leu Arg Met Ser Gln Ser Ala Ile Arg Asn Ala Gln Ala Gln
545                 550                 555                 560

Leu Thr Ser Leu Thr Asn Leu Trp Pro Ala Ser Leu Glu Glu Ala Ser
                565                 570                 575

Ser Ala Glu Arg Leu Ser Phe Glu Thr Asp Tyr Leu Ala Leu Ala Gln
            580                 585                 590

Thr Ser Asn Ala Glu Asn Tyr Ser Glu Ile Val Ala Tyr Val Glu Ser
        595                 600                 605

Gly Ser Thr Asp Ile Asn Pro Leu Leu Arg Ser Gly Val Arg Asn Ala
    610                 615                 620

Thr Thr Arg Arg Phe Leu Arg Gln Phe His Lys Leu Asn Ala Trp Glu
625                 630                 635                 640

Gly Thr Ala Phe Arg Ala Thr Tyr Val Ser Ser Asp Gly Val Ala Cys
                645                 650                 655

Leu Glu Arg Glu Val Gly Ser Val Phe Thr Asp Asn Gly Val Gln Ser
            660                 665                 670

Ala Ser Val Ser Arg Ala Asn Ala Ser Arg Trp Ser Gln Asp Gly Phe
        675                 680                 685

Val Ser Ser Asn Ala Asn Ala Ala Asn His Pro Val Phe Phe Ile Phe
    690                 695                 700

Ala Pro Gly Val Pro Lys Lys Asn Met Phe Thr Gly Phe Leu Gly Asp
705                 710                 715                 720

His Val Ala Ile Pro Pro Gly Thr Cys Val Gln Leu Gly Ala Thr Lys
                725                 730                 735
```

-continued

```
Arg Ile Asn Gly Gln Leu Phe Ala Trp Phe Asp Ala Pro Glu Gln Met
            740                 745                 750

Val Asp Gln Thr Tyr Asp Leu Tyr Thr Gly Glu Gln Glu Leu Trp Val
        755                 760                 765
```

<210> SEQ ID NO 89
<211> LENGTH: 2745
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 89

```
atgactcagc taaaccctgc gggacaaccg cccgcagaac cgacccgaat cgtcaaagct     60

cacattgacc tcatggatcc tgccgaaagc gctgactacg aggcgacccg aatggcattg    120

ctcgcagcga tgcaaagcgg caatgccgcg atcaacctcg aacagattcg gctcaagccc    180

gacccagcgt ccgggttcgg cgaatactgc gctgagaaag ctgcgctacc tcacccggtc    240

caggccgaaa accaggaact cccgtttcag atagacagcg atggcagcgt cagtctggca    300

ttgatgctgc gctataacta cgggttgtcg ctgccgcaat cgcctgacga aacagcgatc    360

aaaaccctgc tcaatacgct ggcagaactt cgcaccagtc aagaactggg gcttattgat    420

cagttcgaca tcaaggccat gctgaccatg caaaatctgc aggatctgaa gcgagcctgc    480

attgagtacc ttggcaccga cggtggcacg ctgctaggca agctgggtgc tgaaataatt    540

gcctcctgcc cactggcaga tgtgcagaac tccccggtga cggttattgc ccggattctc    600

agatcggaac cggcaagggc attggggcaa acgctgctgg cacagcttgg tcggcctgaa    660

gaagaaacgg acgcgtccct gacaacactc gtggaccgga ttttatggta tgccatcagt    720

agcgatcttc atgatccaga aaaccggaag ccaggagaaa ttgccggcta tccattcacc    780

caggccgaaa accagggacg ccgccacgct gacatcctga acgatattca caaccacctg    840

atcaccacgg gcaaggctga gtctgtcaac gaagcaataa ttgcctgctt catacttgca    900

ctcgatgact gcccggaatg gctggtcagc agtgttcccg atgatctgcc atacggctgt    960

acagaggtgt gggtcaactt tcaacatggg gtcacacttg cggaagtcat cgagtttggc   1020

tcgtcacgct ggatgaactt tgaagacctg atcgagctgc cggtgatttt caacaaaaag   1080

atggacaccg aagagcagca agtcgcctat gtcgcaacgc gcatgcccat tcttctgact   1140

tgggcccagg ccaacggtta cattcgtacc cagagcgacc tgccttactc cgaacaagag   1200

atagaacagg ccgccagcgc gtttgaacac tccgagaaac aatcccttga agctgcgaac   1260

gccttgatcc ggaaagcgcc agaacgcaaa gccatggcta tcagtgccat gaaagaagcg   1320

cggaggacgc ctgaaataga aaaaatactt gagcaggaag attactggtt tccgcccatc   1380

gatctcggca tcaggctggc ggtgctacgc aaaaatcaca cgcctgtcta tcgcgatcac   1440

caaggcacgc tctcaccgtc aaatctgcca tacgacccct acggcataaa acacaaggcg   1500

tcgtcgttgc tggagatcta catggcaggt gaaaacattg atgactggag actgccgggg   1560

cgcaacagca acgagggcct gcttcccatc aaccgtgaaa tgcagttgtt gtacaaggcg   1620

ctgccagaca tcaatcaaag gttcgagagt gaatttcagg cttatctggc agatgcccgt   1680

aaggcgtatg cgacgattat cagaaagttg ctgactcacc tgccgctcaa gcaccgcatg   1740

gcgatcgaaa atggtgaggt gtcgctacac tcactcagat tgccgaccaa ggacgtgctg   1800

gcggcgacag agagcgaaaa acatcgggag ccgttgcgag ggcgcacggg ctttgtcatc   1860

aaagctgtct acgagggcaa aaccacgttt tacgaggtgt ttccgttatc gatgattgta   1920

cgctatcgcc ctgatctgga ggcccttctc aagaacggtg tggtcggtat agatttttgg   1980
```

-continued

```
gacattctgc ctcccacccg tataccggta gcggtttata acggaatcac aatgccattt   2040

gatcagggag cctatttgaa cggtcagcta cctgagcctg gggcaagcgc tgtgatgatt   2100

gcagaaacca ttggtgaacg atttgattct tcaagtgcag aggtcgggca acaccagcct   2160

ccgacctcgt tttcaaaacg ctctactggc attgccgaga ccatcacaac atcgcttttc   2220

tacgtcaacg aagatgcact ctttgcacac tgcaaaagcc tcacgcaggt agaaatagat   2280

aacggtgccc caggtgcgct cgaagaggtg tccagctttc tgatacacct gacgccctgg   2340

ccggaaatcg aaaacattct gtccggagag aaagcgctta tgaggggagg agcaatcggt   2400

ctggcgcttt acatgattcc ctatgtggga cccgcgggca agttgctcgc aggcacggca   2460

aaagtcgtta cccgcctggg caaaagcctc ataaccagcg gtagcaaagt ccaggtctcg   2520

aaattgctca tcacggccgg caccaccctg aaagacgccc cgctgatcat gatcagacag   2580

gcccctgaca tgaccagtaa agcaatgact ggcgtttcgc aattcgtcgt gaaacacgtc   2640

acctggaaat ttctggcgat acgtataggt attggtttaa gccgcaggct tgtagccatc   2700

atgagcaggc agcaggccca ggccgcaaag caagaggcca cgtaa                   2745
```

<210> SEQ ID NO 90
<211> LENGTH: 914
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 90

```
Met Thr Gln Leu Asn Pro Ala Gly Gln Pro Pro Ala Glu Pro Thr Arg
  1               5                  10                  15

Ile Val Lys Ala His Ile Asp Leu Met Asp Pro Ala Glu Ser Ala Asp
             20                  25                  30

Tyr Glu Ala Thr Arg Met Ala Leu Leu Ala Ala Met Gln Ser Gly Asn
         35                  40                  45

Ala Ala Ile Asn Leu Glu Gln Ile Arg Leu Lys Pro Asp Pro Ala Ser
     50                  55                  60

Gly Phe Gly Glu Tyr Cys Ala Glu Lys Ala Ala Leu Pro His Pro Val
 65                  70                  75                  80

Gln Ala Glu Asn Gln Glu Leu Pro Phe Gln Ile Asp Ser Asp Gly Ser
                 85                  90                  95

Val Ser Leu Ala Leu Met Leu Arg Tyr Asn Tyr Gly Leu Ser Leu Pro
            100                 105                 110

Gln Ser Pro Asp Glu Thr Ala Ile Lys Thr Leu Leu Asn Thr Leu Ala
        115                 120                 125

Glu Leu Arg Thr Ser Gln Glu Leu Gly Leu Ile Asp Gln Phe Asp Ile
    130                 135                 140

Lys Ala Met Leu Thr Met Gln Asn Leu Gln Asp Leu Lys Arg Ala Cys
145                 150                 155                 160

Ile Glu Tyr Leu Gly Thr Asp Gly Gly Thr Leu Leu Gly Lys Leu Gly
                165                 170                 175

Ala Glu Ile Ile Ala Ser Cys Pro Leu Ala Asp Val Gln Asn Ser Pro
            180                 185                 190

Val Thr Val Ile Ala Arg Ile Leu Arg Ser Glu Pro Ala Arg Ala Leu
        195                 200                 205

Gly Gln Thr Leu Leu Ala Gln Leu Gly Arg Pro Glu Glu Glu Thr Asp
    210                 215                 220

Ala Ser Leu Thr Thr Leu Val Asp Arg Ile Leu Trp Tyr Ala Ile Ser
225                 230                 235                 240
```

-continued

```
Ser Asp Leu His Asp Pro Glu Asn Arg Lys Pro Gly Glu Ile Ala Gly
                245                 250                 255

Tyr Pro Phe Thr Gln Ala Glu Asn Gln Gly Arg Arg His Ala Asp Ile
            260                 265                 270

Leu Asn Asp Ile His Asn His Leu Ile Thr Thr Gly Lys Ala Glu Ser
        275                 280                 285

Val Asn Glu Ala Ile Ile Ala Cys Phe Ile Leu Ala Leu Asp Asp Cys
    290                 295                 300

Pro Glu Trp Leu Val Ser Ser Val Pro Asp Asp Leu Pro Tyr Gly Cys
305                 310                 315                 320

Thr Glu Val Trp Val Asn Phe Gln His Gly Val Thr Leu Ala Glu Val
                325                 330                 335

Ile Glu Phe Gly Ser Ser Arg Trp Met Asn Phe Glu Asp Leu Ile Glu
            340                 345                 350

Leu Pro Val Ile Phe Asn Lys Lys Met Asp Thr Glu Glu Gln Gln Val
        355                 360                 365

Ala Tyr Val Ala Thr Arg Met Pro Ile Leu Leu Thr Trp Ala Gln Ala
    370                 375                 380

Asn Gly Tyr Ile Arg Thr Gln Ser Asp Leu Pro Tyr Ser Glu Gln Glu
385                 390                 395                 400

Ile Glu Gln Ala Ala Ser Ala Phe Glu His Ser Glu Lys Gln Ser Leu
                405                 410                 415

Glu Ala Ala Asn Ala Leu Ile Arg Lys Ala Pro Glu Arg Lys Ala Met
            420                 425                 430

Ala Ile Ser Ala Met Lys Glu Ala Arg Arg Thr Pro Glu Ile Glu Lys
        435                 440                 445

Ile Leu Glu Gln Glu Asp Tyr Trp Phe Pro Pro Ile Asp Leu Gly Ile
    450                 455                 460

Arg Leu Ala Val Leu Arg Lys Asn His Thr Pro Val Tyr Arg Asp His
465                 470                 475                 480

Gln Gly Thr Leu Ser Pro Ser Asn Leu Pro Tyr Asp Pro Tyr Gly Ile
                485                 490                 495

Lys His Lys Ala Ser Ser Leu Leu Glu Ile Tyr Met Ala Gly Glu Asn
            500                 505                 510

Ile Asp Asp Trp Arg Leu Pro Gly Arg Asn Ser Asn Glu Gly Leu Leu
        515                 520                 525

Pro Ile Asn Arg Glu Met Gln Leu Leu Tyr Lys Ala Leu Pro Asp Ile
    530                 535                 540

Asn Gln Arg Phe Glu Ser Glu Phe Gln Ala Tyr Leu Ala Asp Ala Arg
545                 550                 555                 560

Lys Ala Tyr Ala Thr Ile Ile Arg Lys Leu Leu Thr His Leu Pro Leu
                565                 570                 575

Lys His Arg Met Ala Ile Glu Asn Gly Glu Val Ser Leu His Ser Leu
            580                 585                 590

Arg Leu Pro Thr Lys Asp Val Leu Ala Ala Thr Glu Ser Glu Lys His
        595                 600                 605

Arg Glu Pro Leu Arg Gly Arg Thr Gly Phe Val Ile Lys Ala Val Tyr
    610                 615                 620

Glu Gly Lys Thr Thr Phe Tyr Glu Val Phe Pro Leu Ser Met Ile Val
625                 630                 635                 640

Arg Tyr Arg Pro Asp Leu Glu Ala Leu Leu Lys Asn Gly Val Val Gly
                645                 650                 655
```

-continued

```
Ile Asp Phe Trp Asp Ile Leu Pro Pro Thr Arg Ile Pro Val Ala Val
            660                 665                 670

Tyr Asn Gly Ile Thr Met Pro Phe Asp Gln Gly Ala Tyr Leu Asn Gly
        675                 680                 685

Gln Leu Pro Glu Pro Gly Ala Ser Ala Val Met Ile Ala Glu Thr Ile
    690                 695                 700

Gly Glu Arg Phe Asp Ser Ser Ser Ala Glu Val Gly Gln His Gln Pro
705                 710                 715                 720

Pro Thr Ser Phe Ser Lys Arg Ser Thr Gly Ile Ala Glu Thr Ile Thr
                725                 730                 735

Thr Ser Leu Phe Tyr Val Asn Glu Asp Ala Leu Phe Ala His Cys Lys
            740                 745                 750

Ser Leu Thr Gln Val Glu Ile Asp Asn Gly Ala Pro Gly Ala Leu Glu
        755                 760                 765

Glu Val Ser Ser Phe Leu Ile His Leu Thr Pro Trp Pro Glu Ile Glu
    770                 775                 780

Asn Ile Leu Ser Gly Glu Lys Ala Leu Met Arg Gly Gly Ala Ile Gly
785                 790                 795                 800

Leu Ala Leu Tyr Met Ile Pro Tyr Val Gly Pro Ala Gly Lys Leu Leu
                805                 810                 815

Ala Gly Thr Ala Lys Val Val Thr Arg Leu Gly Lys Ser Leu Ile Thr
            820                 825                 830

Ser Gly Ser Lys Val Gln Val Ser Lys Leu Leu Ile Thr Ala Gly Thr
        835                 840                 845

Thr Leu Lys Asp Ala Pro Leu Ile Met Ile Arg Gln Ala Pro Asp Met
    850                 855                 860

Thr Ser Lys Ala Met Thr Gly Val Ser Gln Phe Val Val Lys His Val
865                 870                 875                 880

Thr Trp Lys Phe Leu Ala Ile Arg Ile Gly Ile Gly Leu Ser Arg Arg
                885                 890                 895

Leu Val Ala Ile Met Ser Arg Gln Gln Ala Gln Ala Ala Lys Gln Glu
            900                 905                 910
Ala Thr
```

<210> SEQ ID NO 91
<211> LENGTH: 882
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 91

```
atgtctgtta cttcatctgt cctgcgactg tcgcgcctga gcgtgtcgtt atcacttttg     60

ggcatgctgt cgtctgcact gtttgccggc gcggcattcg ccagcgacga gacgcaactg    120

atcgaatccc tcaacgccta ccgtggccag gcgcagcgct gtggcgagca ggtgtccatg    180

gaactgccgc cgctgagcac cgacccgcgt ctggtgctgc ccgccagtgg caacctgaac    240

ctgcaacagt cgctgacccg cgcgtcttat ccgatggtca ccgtgcaggc gatcagtctg    300

tccggaccgc gagatgcggc gtcggcgttg aaggcggtgc aggagagttt ctgccgcgtg    360

gtgctggacc cgcagttcgt cgatatcggg gtcagccggg acgggcgcga ctggcgcatc    420

gtgctggcgc gctcgctggt ggcatcacgt ctgggtgact ggcaagcaga aggtcagaaa    480

attctggaga tgatcaacac cgcccgtacc caggcgcgtc agtgcggttc gcaatccttc    540

gcggccacta caccgttgag ctggaatcag gtattgggga cggccgcaca aggacactcg    600

caggcaatgg ccaatcagaa cttctttgac cacaaggggc gcgacggccg cacgccgggt    660
```

-continued

gacagggccg agcttgccgg ctatctgggc cagcagatcg gtgagaatat tgccgcaggc 720

caggacactg cccgcaaggt ggtggacggc tggctggtca gcccgggcca ctgcgcaaac 780

ctgatgaccc ccggttttcg cgagctggga gccgcctacg cgatggaccc caaaagtgac 840

gcggggattt actggacagc catgttcggc acgcagcaat ag 882

<210> SEQ ID NO 92
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 92

Met Ser Val Thr Ser Ser Val Leu Arg Leu Ser Arg Leu Ser Val Ser
1 5 10 15

Leu Ser Leu Leu Gly Met Leu Ser Ser Ala Leu Phe Ala Gly Ala Ala
20 25 30

Phe Ala Ser Asp Glu Thr Gln Leu Ile Glu Ser Leu Asn Ala Tyr Arg
35 40 45

Gly Gln Ala Gln Arg Cys Gly Glu Gln Val Ser Met Glu Leu Pro Pro
50 55 60

Leu Ser Thr Asp Pro Arg Leu Val Leu Pro Ala Ser Gly Asn Leu Asn
65 70 75 80

Leu Gln Gln Ser Leu Thr Arg Ala Ser Tyr Pro Met Val Thr Val Gln
85 90 95

Ala Ile Ser Leu Ser Gly Pro Arg Asp Ala Ala Ser Ala Leu Lys Ala
100 105 110

Val Gln Glu Ser Phe Cys Arg Val Val Leu Asp Pro Gln Phe Val Asp
115 120 125

Ile Gly Val Ser Arg Asp Gly Arg Asp Trp Arg Ile Val Leu Ala Arg
130 135 140

Ser Leu Val Ala Ser Arg Leu Gly Asp Trp Gln Ala Glu Gly Gln Lys
145 150 155 160

Ile Leu Glu Met Ile Asn Thr Ala Arg Thr Gln Ala Arg Gln Cys Gly
165 170 175

Ser Gln Ser Phe Ala Ala Thr Thr Pro Leu Ser Trp Asn Gln Val Leu
180 185 190

Gly Thr Ala Ala Gln Gly His Ser Gln Ala Met Ala Asn Gln Asn Phe
195 200 205

Phe Asp His Lys Gly Arg Asp Gly Arg Thr Pro Gly Asp Arg Ala Glu
210 215 220

Leu Ala Gly Tyr Leu Gly Gln Gln Ile Gly Glu Asn Ile Ala Ala Gly
225 230 235 240

Gln Asp Thr Ala Arg Lys Val Val Asp Gly Trp Leu Val Ser Pro Gly
245 250 255

His Cys Ala Asn Leu Met Thr Pro Gly Phe Arg Glu Leu Gly Ala Ala
260 265 270

Tyr Ala Met Asp Pro Lys Ser Asp Ala Gly Ile Tyr Trp Thr Ala Met
275 280 285

Phe Gly Thr Gln Gln
290

<210> SEQ ID NO 93
<211> LENGTH: 1533
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 93

atgccgttat taaactggtc cagacacatg gttcatttaa cagccatcgg ccttatcagc 60

attccggctg cctatgcagc ggacaccctg acccgcgaca atggcgcagc ggtcggcgac 120

aaccagaact ctcagactgc aggcgcccaa gggcctgtcc tgctgcaaga cgtacagctg 180

ctgcagaagc tgcagcgttt tgatcgcgag cgtatcccgg agcgtgtggt ccacgcacgc 240

ggcactggcg tgaaaggcga attcacagcg tccgccgaca tcagcgacct gagcaaggcg 300

accgtcttca aatcgggtga gaagaccccg gtattcgtac gtttttcttc cgtggtccac 360

ggcaaccact cgccagaaac cctgcgcgac ccgcatggct tcgccaccaa gttctacacc 420

gctgatggca actgggacct ggtaggcaac aacttcccga cgttcttcat ccgcgacgcc 480

atcaagttcc cggacatggt gcacgccttc aagcctgacc cgcgtaccaa cctggacaac 540

gactcgcgcc gcttcgactt cttctcgcat gtaccggaag ccacgcgcac gctgaccctg 600

ctgtactcca acgaaggcac accgaccggc tatcgcttca tggacggcaa cggcgttcac 660

gcctacaaac tggtcaacgc caaaggcgaa gtgcactacg tcaagttcca ctggaagacg 720

ctgcaaggca tcaagaacct cgaccctaaa gaagtcgctc aggttcagtc caaggactac 780

agccacctga ccaacgacct ggtcggcgcc atcaagaagg gtgacttccc gaaatgggac 840

ctgtacatcc aggtgctgaa acctgaagac ctggccaagt tcgacttcga cccgctggac 900

gccaccaaaa tctggcctga tgtgccagag aagaaaatcg gccagatggt cctgaacaag 960

aacgtcgaca acttcttcca ggaaaccgag caggtcgcca tggcacccgc caacctggtc 1020

cctggtatcg agccttccga agaccgtctg ctgcaaggtc gagtgttctc ctatgccgac 1080

acgcaaatgt atcgcctggg tgccaacggc ctgagcctgc cggtcaacca gccaaaggtt 1140

gcagtgaaca acggcaatca ggatggcgcg atgaacagcg gcaaaaccac cagcggcgtg 1200

aactacgagc ctagccgtct ggaaccccgt cctgccgatg agaaagcacg ttacagcgag 1260

ctgccaatca gcggcactac ccagcaggcg aagatcacgc gtgagcagaa cttcaagcag 1320

gcgggtgatc tgtatcgctc ttacaacgcg aaagagcaga ccgacctggt gcagagcttc 1380

ggtgaatcgc tggccgacac tgacaccgaa agcaagaaca tcatgctgtc gttcctctac 1440

aaggcagacc ccacctatgg cactcgggta accgaagcgg ccaaaggcga tctggccaag 1500

gtcaagtcac tggctgccag cctgaaagac tga 1533

<210> SEQ ID NO 94
<211> LENGTH: 510
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 94

Met Pro Leu Leu Asn Trp Ser Arg His Met Val His Leu Thr Ala Ile
1 5 10 15

Gly Leu Ile Ser Ile Pro Ala Ala Tyr Ala Ala Asp Thr Leu Thr Arg
20 25 30

Asp Asn Gly Ala Ala Val Gly Asp Asn Gln Asn Ser Gln Thr Ala Gly
35 40 45

Ala Gln Gly Pro Val Leu Leu Gln Asp Val Gln Leu Leu Gln Lys Leu
50 55 60

Gln Arg Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Arg
65 70 75 80

Gly Thr Gly Val Lys Gly Glu Phe Thr Ala Ser Ala Asp Ile Ser Asp
85 90 95

-continued

```
Leu Ser Lys Ala Thr Val Phe Lys Ser Gly Glu Lys Thr Pro Val Phe
            100                 105                 110

Val Arg Phe Ser Ser Val Val His Gly Asn His Ser Pro Glu Thr Leu
        115                 120                 125

Arg Asp Pro His Gly Phe Ala Thr Lys Phe Tyr Thr Ala Asp Gly Asn
    130                 135                 140

Trp Asp Leu Val Gly Asn Asn Phe Pro Thr Phe Phe Ile Arg Asp Ala
145                 150                 155                 160

Ile Lys Phe Pro Asp Met Val His Ala Phe Lys Pro Asp Pro Arg Thr
                165                 170                 175

Asn Leu Asp Asn Asp Ser Arg Arg Phe Asp Phe Phe Ser His Val Pro
            180                 185                 190

Glu Ala Thr Arg Thr Leu Thr Leu Leu Tyr Ser Asn Glu Gly Thr Pro
        195                 200                 205

Thr Gly Tyr Arg Phe Met Asp Gly Asn Gly Val His Ala Tyr Lys Leu
    210                 215                 220

Val Asn Ala Lys Gly Glu Val His Tyr Val Lys Phe His Trp Lys Thr
225                 230                 235                 240

Leu Gln Gly Ile Lys Asn Leu Asp Pro Lys Glu Val Ala Gln Val Gln
                245                 250                 255

Ser Lys Asp Tyr Ser His Leu Thr Asn Asp Leu Val Gly Ala Ile Lys
            260                 265                 270

Lys Gly Asp Phe Pro Lys Trp Asp Leu Tyr Ile Gln Val Leu Lys Pro
        275                 280                 285

Glu Asp Leu Ala Lys Phe Asp Phe Asp Pro Leu Asp Ala Thr Lys Ile
    290                 295                 300

Trp Pro Asp Val Pro Glu Lys Lys Ile Gly Gln Met Val Leu Asn Lys
305                 310                 315                 320

Asn Val Asp Asn Phe Phe Gln Glu Thr Glu Gln Val Ala Met Ala Pro
                325                 330                 335

Ala Asn Leu Val Pro Gly Ile Glu Pro Ser Glu Asp Arg Leu Leu Gln
            340                 345                 350

Gly Arg Val Phe Ser Tyr Ala Asp Thr Gln Met Tyr Arg Leu Gly Ala
        355                 360                 365

Asn Gly Leu Ser Leu Pro Val Asn Gln Pro Lys Val Ala Val Asn Asn
    370                 375                 380

Gly Asn Gln Asp Gly Ala Met Asn Ser Gly Lys Thr Thr Ser Gly Val
385                 390                 395                 400

Asn Tyr Glu Pro Ser Arg Leu Glu Pro Arg Pro Ala Asp Glu Lys Ala
                405                 410                 415

Arg Tyr Ser Glu Leu Pro Ile Ser Gly Thr Thr Gln Gln Ala Lys Ile
            420                 425                 430

Thr Arg Glu Gln Asn Phe Lys Gln Ala Gly Asp Leu Tyr Arg Ser Tyr
        435                 440                 445

Asn Ala Lys Glu Gln Thr Asp Leu Val Gln Ser Phe Gly Glu Ser Leu
    450                 455                 460

Ala Asp Thr Asp Thr Glu Ser Lys Asn Ile Met Leu Ser Phe Leu Tyr
465                 470                 475                 480

Lys Ala Asp Pro Thr Tyr Gly Thr Arg Val Thr Glu Ala Ala Lys Gly
                485                 490                 495

Asp Leu Ala Lys Val Lys Ser Leu Ala Ala Ser Leu Lys Asp
            500                 505                 510
```

-continued

<210> SEQ ID NO 95
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 95

atggggttt cgagctgcgg caaaagtgcc gtcggtgcag aaatcgcccg taacagcggc 60

ggtcgcctga tcgaaggcga tgcgttccat ccccaggcca acatcgacaa gatgagcgcc 120

ggcacccccc tcaccgacga agaccgtgcc ggctggctga cccgtctggg tgaagaactg 180

gccgcagccc ttgccaaggg cgaacatccg gtgctgacct gttcggcact caagctcatt 240

tatcgtgaac gcctgcgtgc ggcggtgccg ggcctgggtt ttgtctttct cgaactgagc 300

aaagagctgg ccaccgagcg ttgcgccaac cggaccgggc atttcatgcc tgcgagtctg 360

gtcgatagcc agttcgcgac cctggaacca ccgatcggcg agccactgac cctggtggtc 420

gatgccagca agcctatcga tgtaattggt gaacaagccg cggcatggtg gaaaggctct 480

cacgcctga 489

<210> SEQ ID NO 96
<211> LENGTH: 162
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 96

Met Gly Val Ser Ser Cys Gly Lys Ser Ala Val Gly Ala Glu Ile Ala
1 5 10 15

Arg Asn Ser Gly Gly Arg Leu Ile Glu Gly Asp Ala Phe His Pro Gln
20 25 30

Ala Asn Ile Asp Lys Met Ser Ala Gly Thr Pro Leu Thr Asp Glu Asp
35 40 45

Arg Ala Gly Trp Leu Thr Arg Leu Gly Glu Glu Leu Ala Ala Ala Leu
50 55 60

Ala Lys Gly Glu His Pro Val Leu Thr Cys Ser Ala Leu Lys Leu Ile
65 70 75 80

Tyr Arg Glu Arg Leu Arg Ala Ala Val Pro Gly Leu Gly Phe Val Phe
85 90 95

Leu Glu Leu Ser Lys Glu Leu Ala Thr Glu Arg Cys Ala Asn Arg Thr
100 105 110

Gly His Phe Met Pro Ala Ser Leu Val Asp Ser Gln Phe Ala Thr Leu
115 120 125

Glu Pro Pro Ile Gly Glu Pro Leu Thr Leu Val Val Asp Ala Ser Lys
130 135 140

Pro Ile Asp Val Ile Gly Glu Gln Ala Ala Ala Trp Trp Lys Gly Ser
145 150 155 160
His Ala

<210> SEQ ID NO 97
<211> LENGTH: 3405
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 97

atgcgaccgg tgtctatgtt ttccctgcgt tccatttgtg ctgccgcact gtttgcgctt 60

tgcctgtcta tcttcccggc gctggccgcc gagccgccca cccgcgatgc cgtgcagcaa 120

agcctcgaca agattgccga ccgcaagctg ccggatgccg atcagaaggc cttgcagcag 180

gtgcttgagc agacgctggc gtttctcaac agcaaagacg acagcgagca aaagctgacc 240

-continued

```
gcgctcaagc agcagctggc tcaagcgcca aaacagacct cggacaacca gcgcgagctg    300

gcccggttga aagaaagcaa agtcgttgcc gttgcacagc gctacggtgg cctcgatgtg    360

ccgcaactgg agcaactgct cagccagcgc agcacccagc aaagtgatct gcaaagcgag    420

cttaacgacg ccaacagcct ggccatcacc gcgcaaaccc ggccggagcg ggcgcagact    480

gaaatcagcg ccaatcagac acgcatccag cagatcaatg ccatcctcaa gaatggcaaa    540

gacaacggca agaccctgag tgccgatcag cgcaatctgc tcaatgcgga actggcctcg    600

atcaacgcgc tgaacctgct gcgccgtcag gaactggccg gcaacagcca gttacaggac    660

ctgggcaaca gccagcacga cttgctgacc gaaaaagtcg cccgccagga gcaggaaatt    720

caggacctgc aaaccctgat caacgacaag cgccgagccc agtcgcagaa aaccgtggcg    780

gacctgtctc tggaagcgca gaaatccggt ggcagcagcc tcctggcgac cgagagcgcc    840

gccaacctca agctgtccga ttacctgctg cgcggcaccg accgtctcaa cgagctgacc    900

cagcaaaacc tcaagaccaa gcagcaactg gacaacctga cgcagaccga tcaagccctc    960

agcgagcaga tcaacgtgct gagcggcagc ctgctgctgt ccaagattct ctacaagcaa   1020

aaacagtcgt tgccgcacct ggaactggac aaaggcctgg ctgacgaaat cgccaacatc   1080

cgcctttatc agttcgacat caatcagcaa cgcgagcaga tgagcacacc gaccgcttac   1140

gtcgaacgac tgctcgccac ccagcccccg gaaaatatca ccccgcaact gcgcaggacg   1200

ctgcttgatc tggccatcac ccgcagcgac ctgctcgaac gcctgaaccg cgagctgagc   1260

gcgttgctca acgagtccat cacgctgcaa ttgaaccaga agcagttgac cagtaccgcc   1320

gtcggcctgc gctccacgct ggacgagcag atgttctgga tccccagcaa caagccgctg   1380

gatctggagt ggttccagaa catctggccg cgcctgcaaa aacaggtcgc gaccctgccc   1440

tggacgtcca gcctcagcga gctgtcggac ggcttgacac aacgcccgct gctgtttctg   1500

ccattgttac tgctgatcgg tgtactgacc tggaggcgca aggcgcttta ccagaagctc   1560

aaccggctgc acgccgacat cggccacttc aaacgcgaca gtcagtggaa aaccccgttg   1620

gcgctgctga tcaacgtgct gctggccatg ccggtcgcat tggggctggc gctgtgcggc   1680

tacgccttgc aaatcgatgc gcgcgggcaa aacgccaacc ttggcgaggc cttgctgcag   1740

atcgcgctgg cctggctagt gttctacacc gcctaccgcg tgctggcccc gtccggcgtt   1800

gcgcaactgc actttcgctg ggaaccggcg caggtcgcgt tcttgcgcgg ctgggttcgt   1860

cgcctggggt tggtggtgct ggcgctggtc gccgtggtgg cggtcgccga gcatcaaccg   1920

gccgcgctgg ccgacgacgt gctgggtatc ggcgtggtgc tgacctgtta cgcgctgatg   1980

acctggctgc tgggccgatt gctgctctcc agccctacgc accacaacgc gtcgctgttc   2040

cgcaagacgc tgggtgtggc gttcacggca ttgccggtcg cgctgtttct ggcggtgtgc   2100

ttcggctact actacaccgc actcaagctc agcgaccgtc tgatcgacac gctgtacctg   2160

atgatgatct ggctgatggt cgaggccacc ttcgttcgtg gtctgggcgt tgccgcgcgg   2220

cgactggcct accagcgtgc gctggccaaa cgtcaggctg cgcgagaaaa cggtgacagc   2280

gacatccccg tcgaagaacc gaaactggac atcgaacagg tcaaccagca gtcgctgcgc   2340

ctgattcgtc tggccttgct ggctggtttc gtcggcgcgt tgtacctggt ctgggccgag   2400

ctgatcacgg tgttcgccta cctggacaac atcatcctct acgaatacac aagcggcaca   2460

ggcgccaaca tgagcatggt gccgatcagc ctgagcgact tcctcggtgc cggggtcatc   2520

atcgtcatta cctttgtgct ggcgggcaac ctgcccggct tgctcgaggt gctggttctg   2580

tcacgcatga acctggcgca aggcagcgcc tatgcgacca ccacgctgct ctcctacacc   2640
```

-continued

```
atcgccggca tcggctttgt gaccacgctg tccacattag gcgtgagctg ggacaagctg   2700

cagtggctgg tcgcagcgct gtcggtgggc ctggggttcg gcatgcagga gatcttcgcc   2760

aacttcattt ccggcatcat gatcctcttc gagcgcccgg tacggatcgg cgacaccatc   2820

accatcggcg ccctgtcggg tacggtcagc aagatccgca tccgcgccac gaccatcacc   2880

gacttcgacc gcaaggacat tatcgtcccg aacaagacct tcatcaccgg ccagctcatc   2940

aactggtcac tgactgacac cgtcacccgc gtaacgctca agctgggtgt ggattacggc   3000

tcggacctgg acctcgtgcg ctccctgctg ctgcaagccg cacgggaaaa ccctcgggtg   3060

ctcaaggagc cagagcccat tgtctacttc ctgaacttcg gcgaaagcac cctcgaccac   3120

gaactgcgca tgcacgttcg cgacctgggc gaccgcaacc cggtactcga cgagatcaac   3180

cgcttcatca accgcgagtt caagaaacag cacatcaaca tctcgttccg ccagatggag   3240

atctacctca aaaacaccca gggcctggaa tacaaactgg tgcccgccga accaggcgaa   3300

aagcacggcg caccggctgg gcaaaccacg ctgcaaccgg taaacaccaa agtagccccg   3360

gcaaccaaag atgcgccaga gccgccggag ttgaggctgg actga                   3405
```

<210> SEQ ID NO 98
<211> LENGTH: 1134
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 98

```
Met Arg Pro Val Ser Met Phe Ser Leu Arg Ser Ile Cys Ala Ala Ala
  1               5                  10                  15

Leu Phe Ala Leu Cys Leu Ser Ile Phe Pro Ala Leu Ala Ala Glu Pro
             20                  25                  30

Pro Thr Arg Asp Ala Val Gln Gln Ser Leu Asp Lys Ile Ala Asp Arg
         35                  40                  45

Lys Leu Pro Asp Ala Asp Gln Lys Ala Leu Gln Gln Val Leu Glu Gln
     50                  55                  60

Thr Leu Ala Phe Leu Asn Ser Lys Asp Asp Ser Glu Gln Lys Leu Thr
 65                  70                  75                  80

Ala Leu Lys Gln Gln Leu Ala Gln Ala Pro Lys Gln Thr Ser Asp Asn
                 85                  90                  95

Gln Arg Glu Leu Ala Arg Leu Lys Glu Ser Lys Val Val Ala Val Ala
            100                 105                 110

Gln Arg Tyr Gly Gly Leu Asp Val Pro Gln Leu Glu Gln Leu Leu Ser
        115                 120                 125

Gln Arg Ser Thr Gln Gln Ser Asp Leu Gln Ser Glu Leu Asn Asp Ala
    130                 135                 140

Asn Ser Leu Ala Ile Thr Ala Gln Thr Arg Pro Glu Arg Ala Gln Thr
145                 150                 155                 160

Glu Ile Ser Ala Asn Gln Thr Arg Ile Gln Gln Ile Asn Ala Ile Leu
                165                 170                 175

Lys Asn Gly Lys Asp Asn Gly Lys Thr Leu Ser Ala Asp Gln Arg Asn
            180                 185                 190

Leu Leu Asn Ala Glu Leu Ala Ser Ile Asn Ala Leu Asn Leu Leu Arg
        195                 200                 205

Arg Gln Glu Leu Ala Gly Asn Ser Gln Leu Gln Asp Leu Gly Asn Ser
    210                 215                 220

Gln His Asp Leu Leu Thr Glu Lys Val Ala Arg Gln Glu Gln Glu Ile
225                 230                 235                 240
```

-continued

```
Gln Asp Leu Gln Thr Leu Ile Asn Asp Lys Arg Arg Ala Gln Ser Gln
                245                 250                 255

Lys Thr Val Ala Asp Leu Ser Leu Glu Ala Gln Lys Ser Gly Gly Ser
            260                 265                 270

Ser Leu Leu Ala Thr Glu Ser Ala Ala Asn Leu Lys Leu Ser Asp Tyr
        275                 280                 285

Leu Leu Arg Gly Thr Asp Arg Leu Asn Glu Leu Thr Gln Gln Asn Leu
    290                 295                 300

Lys Thr Lys Gln Gln Leu Asp Asn Leu Thr Gln Thr Asp Gln Ala Leu
305                 310                 315                 320

Ser Glu Gln Ile Asn Val Leu Ser Gly Ser Leu Leu Leu Ser Lys Ile
                325                 330                 335

Leu Tyr Lys Gln Lys Gln Ser Leu Pro His Leu Glu Leu Asp Lys Gly
            340                 345                 350

Leu Ala Asp Glu Ile Ala Asn Ile Arg Leu Tyr Gln Phe Asp Ile Asn
        355                 360                 365

Gln Gln Arg Glu Gln Met Ser Thr Pro Thr Ala Tyr Val Glu Arg Leu
    370                 375                 380

Leu Ala Thr Gln Pro Pro Glu Asn Ile Thr Pro Gln Leu Arg Arg Thr
385                 390                 395                 400

Leu Leu Asp Leu Ala Ile Thr Arg Ser Asp Leu Leu Glu Arg Leu Asn
                405                 410                 415

Arg Glu Leu Ser Ala Leu Leu Asn Glu Ser Ile Thr Leu Gln Leu Asn
            420                 425                 430

Gln Lys Gln Leu Thr Ser Thr Ala Val Gly Leu Arg Ser Thr Leu Asp
        435                 440                 445

Glu Gln Met Phe Trp Ile Pro Ser Asn Lys Pro Leu Asp Leu Glu Trp
    450                 455                 460

Phe Gln Asn Ile Trp Pro Arg Leu Gln Lys Gln Val Ala Thr Leu Pro
465                 470                 475                 480

Trp Thr Ser Ser Leu Ser Glu Leu Ser Asp Gly Leu Thr Gln Arg Pro
                485                 490                 495

Leu Leu Phe Leu Pro Leu Leu Leu Leu Ile Gly Val Leu Thr Trp Arg
            500                 505                 510

Arg Lys Ala Leu Tyr Gln Lys Leu Asn Arg Leu His Ala Asp Ile Gly
        515                 520                 525

His Phe Lys Arg Asp Ser Gln Trp Lys Thr Pro Leu Ala Leu Leu Ile
    530                 535                 540

Asn Val Leu Leu Ala Met Pro Val Ala Leu Gly Leu Ala Leu Cys Gly
545                 550                 555                 560

Tyr Ala Leu Gln Ile Asp Ala Arg Gly Gln Asn Ala Asn Leu Gly Glu
                565                 570                 575

Ala Leu Leu Gln Ile Ala Leu Ala Trp Leu Val Phe Tyr Thr Ala Tyr
            580                 585                 590

Arg Val Leu Ala Pro Ser Gly Val Ala Gln Leu His Phe Arg Trp Glu
        595                 600                 605

Pro Ala Gln Val Ala Phe Leu Arg Gly Trp Val Arg Arg Leu Gly Leu
    610                 615                 620

Val Val Leu Ala Leu Val Ala Val Val Ala Val Ala Glu His Gln Pro
625                 630                 635                 640

Ala Ala Leu Ala Asp Asp Val Leu Gly Ile Gly Val Val Leu Thr Cys
                645                 650                 655
```

-continued

```
Tyr Ala Leu Met Thr Trp Leu Leu Gly Arg Leu Leu Leu Ser Ser Pro
            660                 665                 670

Thr His His Asn Ala Ser Leu Phe Arg Lys Thr Leu Gly Val Ala Phe
        675                 680                 685

Thr Ala Leu Pro Val Ala Leu Phe Leu Ala Val Cys Phe Gly Tyr Tyr
    690                 695                 700

Tyr Thr Ala Leu Lys Leu Ser Asp Arg Leu Ile Asp Thr Leu Tyr Leu
705                 710                 715                 720

Met Met Ile Trp Leu Met Val Glu Ala Thr Phe Val Arg Gly Leu Gly
                725                 730                 735

Val Ala Ala Arg Arg Leu Ala Tyr Gln Arg Ala Leu Ala Lys Arg Gln
            740                 745                 750

Ala Ala Arg Glu Asn Gly Asp Ser Asp Ile Pro Val Glu Glu Pro Lys
        755                 760                 765

Leu Asp Ile Glu Gln Val Asn Gln Gln Ser Leu Arg Leu Ile Arg Leu
    770                 775                 780

Ala Leu Leu Ala Gly Phe Val Gly Ala Leu Tyr Leu Val Trp Ala Glu
785                 790                 795                 800

Leu Ile Thr Val Phe Ala Tyr Leu Asp Asn Ile Ile Leu Tyr Glu Tyr
                805                 810                 815

Thr Ser Gly Thr Gly Ala Asn Met Ser Met Val Pro Ile Ser Leu Ser
            820                 825                 830

Asp Phe Leu Gly Ala Gly Val Ile Ile Val Ile Thr Phe Val Leu Ala
        835                 840                 845

Gly Asn Leu Pro Gly Leu Leu Glu Val Leu Val Leu Ser Arg Met Asn
    850                 855                 860

Leu Ala Gln Gly Ser Ala Tyr Ala Thr Thr Thr Leu Leu Ser Tyr Thr
865                 870                 875                 880

Ile Ala Gly Ile Gly Phe Val Thr Thr Leu Ser Thr Leu Gly Val Ser
                885                 890                 895

Trp Asp Lys Leu Gln Trp Leu Val Ala Ala Leu Ser Val Gly Leu Gly
            900                 905                 910

Phe Gly Met Gln Glu Ile Phe Ala Asn Phe Ile Ser Gly Ile Met Ile
        915                 920                 925

Leu Phe Glu Arg Pro Val Arg Ile Gly Asp Thr Ile Thr Ile Gly Ala
    930                 935                 940

Leu Ser Gly Thr Val Ser Lys Ile Arg Ile Arg Ala Thr Thr Ile Thr
945                 950                 955                 960

Asp Phe Asp Arg Lys Asp Ile Ile Val Pro Asn Lys Thr Phe Ile Thr
                965                 970                 975

Gly Gln Leu Ile Asn Trp Ser Leu Thr Asp Thr Val Thr Arg Val Thr
            980                 985                 990

Leu Lys Leu Gly Val Asp Tyr Gly Ser Asp Leu Asp Leu Val Arg Ser
        995                1000                1005

Leu Leu Leu Gln Ala Ala Arg Glu Asn Pro Arg Val Leu Lys Glu Pro
   1010                1015                1020

Glu Pro Ile Val Tyr Phe Leu Asn Phe Gly Glu Ser Thr Leu Asp His
1025                1030                1035                1040

Glu Leu Arg Met His Val Arg Asp Leu Gly Asp Arg Asn Pro Val Leu
               1045                1050                1055

Asp Glu Ile Asn Arg Phe Ile Asn Arg Glu Phe Lys Lys Gln His Ile
           1060                1065                1070
```

-continued

```
Asn Ile Ser Phe Arg Gln Met Glu Ile Tyr Leu Lys Asn Thr Gln Gly
       1075                1080                1085

Leu Glu Tyr Lys Leu Val Pro Ala Glu Pro Gly Glu Lys His Gly Ala
   1090                1095                1100

Pro Ala Gly Gln Thr Thr Leu Gln Pro Val Asn Thr Lys Val Ala Pro
1105                1110                1115                1120

Ala Thr Lys Asp Ala Pro Glu Pro Pro Glu Leu Arg Leu Asp
               1125                1130
```

<210> SEQ ID NO 99
<211> LENGTH: 1113
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 99

```
atgtcaacgt tgaatcatac gtctgctgta aattgccgcg tcagttttga tggtgaccgt     60

tgctatgtag acacccccat ccagatcatg ccgggtgagc gatgggctgt aaatatcgta    120

cctaacgatt tagtcacaat ccactacgag gccgccagca atcacgacta ccctttgctg    180

ctggccagca taaaaaatct gtttaccgat gagcgttgtg tcgtgctaaa gcccggcctt    240

acacagcaag ctttgaacat gtatttttca gaggttaaca gccttaaacc taacgcgact    300

catgttcgct tgttgcatcg agcgcagcgt atttttctag aaaacatgat ccgtagcgta    360

cagataacct cgcaaggtat cagcgtcact ttcgcaaccg ccgaattcaa aaattataac    420

taccagctaa aggtggataa atatactttt gcaaggcttg acaaggggta ccctctctat    480

tcggagctgg ttgaaaacac ctggataacg aaattatccg tagcccataa tattctgtat    540

tccatctctg tgagcctgga ccactcaagc acaccttata cacttttttc aggaaccctc    600

gcggaagaca atatagtcca gccgatacgg gcgcttttca ccgacaacac catgactcaa    660

ctcacctcct tggccgatca gaaaaccgtg gatgccttgt atacgacggt caatggcaac    720

ccggttatca gcatcaaaaa acgcgcagat tatcggtctt atctgaacat cgcacagaag    780

ttactgcttc caagaaccta caccaaagta gtacggacag tgagcagcct gtctgtgcat    840

tttacggggg aggcgtacaa acaattcaac tacaagatgc ttgtcaacaa tgcttatgca    900

tccgagatca cccgagggaa ggcttattac tccagcgtga gcaatggggt gtggaccact    960

tccggtacgc atgacagcga cgacaactgc aaagtcactt gtgattacaa gggcgcaacc   1020

tacgtcctgt acgagagtaa tgcggcagat agacgcactg aaacctgggc acaagacccg   1080

tacgttactc attgcgaccc gagagacctg taa                                1113
```

<210> SEQ ID NO 100
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 100

```
Met Ser Thr Leu Asn His Thr Ser Ala Val Asn Cys Arg Val Ser Phe
  1               5                  10                  15

Asp Gly Asp Arg Cys Tyr Val Asp Thr Pro Ile Gln Ile Met Pro Gly
             20                  25                  30

Glu Arg Trp Ala Val Asn Ile Val Pro Asn Asp Leu Val Thr Ile His
         35                  40                  45

Tyr Glu Ala Ala Ser Asn His Asp Tyr Pro Leu Leu Leu Ala Ser Ile
     50                  55                  60
```

-continued

```
Lys Asn Leu Phe Thr Asp Glu Arg Cys Val Val Leu Lys Pro Gly Leu
 65                  70                  75                  80

Thr Gln Gln Ala Leu Asn Met Tyr Phe Ser Glu Val Asn Ser Leu Lys
                 85                  90                  95

Pro Asn Ala Thr His Val Arg Leu Leu His Arg Ala Gln Arg Ile Phe
            100                 105                 110

Leu Glu Asn Met Ile Arg Ser Val Gln Ile Thr Ser Gln Gly Ile Ser
        115                 120                 125

Val Thr Phe Ala Thr Ala Glu Phe Lys Asn Tyr Asn Tyr Gln Leu Lys
    130                 135                 140

Val Asp Lys Tyr Thr Phe Ala Arg Leu Asp Lys Gly Tyr Pro Leu Tyr
145                 150                 155                 160

Ser Glu Leu Val Glu Asn Thr Trp Ile Thr Lys Leu Ser Val Ala His
                165                 170                 175

Asn Ile Leu Tyr Ser Ile Ser Val Ser Leu Asp His Ser Ser Thr Pro
            180                 185                 190

Tyr Thr Leu Phe Ser Gly Thr Leu Ala Glu Asp Asn Ile Val Gln Pro
        195                 200                 205

Ile Arg Ala Leu Phe Thr Asp Asn Thr Met Thr Gln Leu Thr Ser Leu
    210                 215                 220

Ala Asp Gln Lys Thr Val Asp Ala Leu Tyr Thr Thr Val Asn Gly Asn
225                 230                 235                 240

Pro Val Ile Ser Ile Lys Lys Arg Ala Asp Tyr Arg Ser Tyr Leu Asn
                245                 250                 255

Ile Ala Gln Lys Leu Leu Leu Pro Arg Thr Tyr Thr Lys Val Val Arg
            260                 265                 270

Thr Val Ser Ser Leu Ser Val His Phe Thr Gly Glu Ala Tyr Lys Gln
        275                 280                 285

Phe Asn Tyr Lys Met Leu Val Asn Asn Ala Tyr Ala Ser Glu Ile Thr
    290                 295                 300

Arg Gly Lys Ala Tyr Tyr Ser Ser Val Ser Asn Gly Val Trp Thr Thr
305                 310                 315                 320

Ser Gly Thr His Asp Ser Asp Asp Asn Cys Lys Val Thr Cys Asp Tyr
                325                 330                 335

Lys Gly Ala Thr Tyr Val Leu Tyr Glu Ser Asn Ala Ala Asp Arg Arg
            340                 345                 350

Thr Glu Thr Trp Ala Gln Asp Pro Tyr Val Thr His Cys Asp Pro Arg
        355                 360                 365

Asp Leu
    370
```

<210> SEQ ID NO 101
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 101

```
atgcgcctga tcgcgcagat tctgcccggc ctgccggaaa acaccactta cagcgccgcc     60

gctgcgtcca acaccctggc gcgggccatg cccaacgcca ttcgcaatgc gctgggcacc    120

ctggggctgg tggctgcgcg cacccagcca agcatctttc cgttgccgtc gcgcaacgtc    180

agcggtggcg aaaaagagga cgacctggag attctgctca aactcgcggc cgccgctgtt    240

tcgcgcctgc aaagccacca gttgggcggc ctggagcaga cccgtaccaa tgccgatggc    300

actcaggtga ctacatggca actggaagtg ccgatgcgca acgcccatga catcgtgccg    360
```

-continued

ttgcaggtca aggtgcagcg cgaagacaag cctgatcagg acgccaccga agaccgcgac 420

gatatcgaga tcaaggaaac ccgtgaaaaa ctctggaaag tcgatctggc tttcgacctg 480

gagccgcttg gccccatgca ggtgcatgcg caactgctgc gcggcacgct gtccagccag 540

ttatgggccg agcgcccgga tagcgcaaca ctgatcgaac atgaactggg gcatttgcgc 600

gagcgcctga ttgcctgcgg cctggccgtc ggggaactgg cgtgcagcca tggcgttccg 660

ccgcaagggc cgcgcaccgc cctcgaacaa cgctggatcg acgagaacgc ctga 714

<210> SEQ ID NO 102
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 102

Met Arg Leu Ile Ala Gln Ile Leu Pro Gly Leu Pro Glu Asn Thr Thr
1 5 10 15

Tyr Ser Ala Ala Ala Ala Ser Asn Thr Leu Ala Arg Ala Met Pro Asn
20 25 30

Ala Ile Arg Asn Ala Leu Gly Thr Leu Gly Leu Val Ala Ala Arg Thr
35 40 45

Gln Pro Ser Ile Phe Pro Leu Pro Ser Arg Asn Val Ser Gly Gly Glu
50 55 60

Lys Glu Asp Asp Leu Glu Ile Leu Leu Lys Leu Ala Ala Ala Ala Val
65 70 75 80

Ser Arg Leu Gln Ser His Gln Leu Gly Gly Leu Glu Gln Thr Arg Thr
85 90 95

Asn Ala Asp Gly Thr Gln Val Thr Thr Trp Gln Leu Glu Val Pro Met
100 105 110

Arg Asn Ala His Asp Ile Val Pro Leu Gln Val Lys Val Gln Arg Glu
115 120 125

Asp Lys Pro Asp Gln Asp Ala Thr Glu Asp Arg Asp Asp Ile Glu Ile
130 135 140

Lys Glu Thr Arg Glu Lys Leu Trp Lys Val Asp Leu Ala Phe Asp Leu
145 150 155 160

Glu Pro Leu Gly Pro Met Gln Val His Ala Gln Leu Leu Arg Gly Thr
165 170 175

Leu Ser Ser Gln Leu Trp Ala Glu Arg Pro Asp Ser Ala Thr Leu Ile
180 185 190

Glu His Glu Leu Gly His Leu Arg Glu Arg Leu Ile Ala Cys Gly Leu
195 200 205

Ala Val Gly Glu Leu Ala Cys Ser His Gly Val Pro Pro Gln Gly Pro
210 215 220

Arg Thr Ala Leu Glu Gln Arg Trp Ile Asp Glu Asn Ala
225 230 235

<210> SEQ ID NO 103
<211> LENGTH: 690
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 103

atgagtagcg tcgcagcact gatcaccata tcgactggac agacgcagtt cgttaaagtc 60

gcgcggacgt cattttctgt gctacgaatc cccctcgccg gcagatgtcg tgtccgggat 120

cagttgacca ctacaataaa gacagagcag aaacccataa aaataggggg aagagacgtg 180

-continued

agcctaaatg atcacttgaa aaaagcattg aattctgatt ccagcgacga gcttgatgaa 240

atcaccgacc tttatgtgac gttgcctgca gaggtcttca gttgcttgac catttcactc 300

gaagggaatt ggaaggaaat tgatagcgtc tggtctgctc ggttagacgc agcagattca 360

aagaataata caaaatgtca cgtccatatc gccaaaacca agcatcgatc ctcaaaaagc 420

aaacaggttt cttggaacag tgatggtagc cggcatgata aaaaaacatt cgatgtaacg 480

ctgggacaga gcagaaaggc ccaggcgata gctaggaaat ttttaggcct tggcgagtcc 540

ataagccttg aaagcaaaga ttccaagcag atggttgaaa gacctctact cagcactgct 600

acatcctttt cgaatgatgg aaaagaggtg aaggtcgagt tctacgtgga agaatccacc 660

gcccaccttc ccgcatggtt acgatggtag 690

<210> SEQ ID NO 104
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 104

Met Ser Ser Val Ala Ala Leu Ile Thr Ile Ser Thr Gly Gln Thr Gln
1 5 10 15

Phe Val Lys Val Ala Arg Thr Ser Phe Ser Val Leu Arg Ile Pro Leu
20 25 30

Ala Gly Arg Cys Arg Val Arg Asp Gln Leu Thr Thr Thr Ile Lys Thr
35 40 45

Glu Gln Lys Pro Ile Lys Ile Gly Gly Arg Asp Val Ser Leu Asn Asp
50 55 60

His Leu Lys Lys Ala Leu Asn Ser Asp Ser Ser Asp Glu Leu Asp Glu
65 70 75 80

Ile Thr Asp Leu Tyr Val Thr Leu Pro Ala Glu Val Phe Ser Cys Leu
85 90 95

Thr Ile Ser Leu Glu Gly Asn Trp Lys Glu Ile Asp Ser Val Trp Ser
100 105 110

Ala Arg Leu Asp Ala Ala Asp Ser Lys Asn Asn Thr Lys Cys His Val
115 120 125

His Ile Ala Lys Thr Lys His Arg Ser Ser Lys Ser Lys Gln Val Ser
130 135 140

Trp Asn Ser Asp Gly Ser Arg His Asp Lys Lys Thr Phe Asp Val Thr
145 150 155 160

Leu Gly Gln Ser Arg Lys Ala Gln Ala Ile Ala Arg Lys Phe Leu Gly
165 170 175

Leu Gly Glu Ser Ile Ser Leu Glu Ser Lys Asp Ser Lys Gln Met Val
180 185 190

Glu Arg Pro Leu Leu Ser Thr Ala Thr Ser Phe Ser Asn Asp Gly Lys
195 200 205

Glu Val Lys Val Glu Phe Tyr Val Glu Glu Ser Thr Ala His Leu Pro
210 215 220

Ala Trp Leu Arg Trp
225

<210> SEQ ID NO 105
<211> LENGTH: 2949
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 105

atgaagccaa tccatactgc ccgatacaac gcctggaatc agttggagca ggagaccgcc 60

catgactggc tgggggccaa acccttggcc agcagcaccc ttggctaccg ctacgatgac 120

tggaaccagc gatgctgcac cacgaccgat gacaacgtac agacttatga gtattcagac 180

ccgatcggca gcgacgtaca taaaggccca atccagaaaa cctggaaaca gagtggcgac 240

ccggagggcc gcatcagtgg ccgcagcgaa acctggctga atctgttcgg caaaccggac 300

cggatccgga cgctgaccgc tggtaaaacg ggtcgcagcc gcacgcacag catgagccgc 360

agccggaacc tgaccacgac tgagcaggaa ctgagcaggc agacctttct gtacgacggg 420

ctgggacgct gcaccgagca gcgcgatgca ctccagcaaa gcaccctgtt cagctacgac 480

aactggtcac gcatggtctc ctccacgctt gcagacggca gcgtcatcaa ccggagttat 540

gcgccgcaaa gcagcagtga gctggcaacg atgctcgagg tcgtgcacca gaacggcacc 600

accagaaccg tggcaggtac acagaaattt gacgggcttg agcgtgtgac gcagaccaaa 660

acaggtgacc gcgtcgaaca gttcaactac gacgccggtg agatgcagcc caggtcgcgc 720

acaacagccg ggctggacaa catcaacttt acctacactc gggcgctcac tgatcagatt 780

ttttccagca cggctccgga tgaaacggcc aaattcgatt atgacaagac cagtgcccgc 840

ctcatcgaag cgacgaaccc gcaaggcacg cgcacttacc gctatgacgt gcacaatcaa 900

ctgacgggag agacttggga caatctgctg ggtcaggctt gggaaacccg acaccaatca 960

tcgctgctgg gtcggccgat caagcgcacc gatctcaaaa aaggcgaggc ggcgggcgca 1020

gagacccgtt acgactacga cacgctcggc agaatcaggt ttatcaacca gagcaacctg 1080

cgcaccacaa tcgactatga cgtgctgggc cagctctgca aggtggccac cgaggacctg 1140

caggccggaa ctggcgtgat catcgacatg gaatacgacg accagggaca ggaaattctc 1200

agaacccaga ccgcaagcaa ccaagcggcg ttgaccttga ctcaaacgtg ggcagtggac 1260

gggcttttga aaacccgcga cctgcaacag gcgggtagcc ccctgctgca cgaaacgttt 1320

agctacgacc ccagaggccg cctgacactg gtgaattacc tgggtagcag cttgccgaga 1380

gacgaactgc aaagggagat gaccagacaa atattcagct tcgacgagct ggacaacatt 1440

acgctatgcc agaccaggtt taccgatggc acctctgagc gagcagcttt caaatacggc 1500

agccccggcg acgataagca taaagaccgc tgccagcttt tgagtattgc ctacacgccg 1560

cccagaaaaa caccggaccc gacattcagt tacgacgcca acggtaacca gcttaaagac 1620

gagcatggca acagtctgca ttacgatagc cagagccgcc tgctgcaggt cgcagaaacc 1680

ggcggtgccc ctatcagcca ataccgttat gacggccaca atcaactggt cgccaccagg 1740

gatggcaatg aaagcgagat tttgcggttc tatgagggtc atcaactgag cagcacggtg 1800

caggaagatc aacgcactca gtacctgcat ctcggcgaac agccgctggg ccagcagatt 1860

gtggacgacg ccgagcaaac cctgttgcta ctgactgacg caaaccagag cgttatgggt 1920

gaatttcaac aaggccagct gcgcaaggcg gtctacagtg cctacgggga gcgccacagc 1980

gaggaggcgc tgctgagcac tgccgggttt aacggtgaag tacgcgaagc cgccaacggc 2040

tggtatctgt tgggcaatgg ctaccgggcc tacaaccctc tcctgatgcg cttccacagc 2100

ccggattttc tcagcccctt cgccgaaggc ggcgtcaacc cctacaccta ctgcctgggc 2160

aaccccatcg ccctgcgcga cccgacagga catgatgcca gcggtcagac tggccggttg 2220

agacggcccg atgagggggc tttgccaatg caacaaggtg gcggagatat catgggttgg 2280

gtgggtgtag gaataggcgt tgttttcacc gtattgggcg ttgccgctac catagccacg 2340

-continued

```
ttaggaacag ccacaccggt taccggcccg gtaactgtcc tgggcatttc catgaccgcc   2400

agcgctgccg cggccgtttc gacagtctcg accggtgcgt tgatcgtcgg tacggcattg   2460

acagcggctt caactacggc caatacagtt gccattgtaa ataacgatca gacggccgga   2520

gaagtcggcg gctggttggg tattgccgct gtgcccgttg gcttggtagg gtttggcgcg   2580

ggggctgtgg tggcgagggc agttgcggct gcggctaaag ttgcggctgc caacgctggt   2640

acgatcggtg tccgcagcgt cagcagaata ggcctcgctg ctgctggtgc ccgcagaacc   2700

atttccagcg ctgccagcag cgctcggcgc caaatcagca acatgttagg cagaatctta   2760

ccccgtgctc taaacaggac tgctgctact gcacgccgga ttccaagcgt tacaagtggc   2820

ggatcaggac cagggccatc attatttaca cagactacct ttaacgaatc gattgggatg   2880

acgcagacca ctatttttc aacgaatgcg agcggaatcc caccggccac gcaggtaact   2940

cgaatctag                                                          2949
```

<210> SEQ ID NO 106
<211> LENGTH: 982
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 106

```
Met Lys Pro Ile His Thr Ala Arg Tyr Asn Ala Trp Asn Gln Leu Glu
  1               5                  10                  15

Gln Glu Thr Ala His Asp Trp Leu Gly Ala Lys Pro Leu Ala Ser Ser
             20                  25                  30

Thr Leu Gly Tyr Arg Tyr Asp Asp Trp Asn Gln Arg Cys Cys Thr Thr
         35                  40                  45

Thr Asp Asp Asn Val Gln Thr Tyr Glu Tyr Ser Asp Pro Ile Gly Ser
     50                  55                  60

Asp Val His Lys Gly Pro Ile Gln Lys Thr Trp Lys Gln Ser Gly Asp
 65                  70                  75                  80

Pro Glu Gly Arg Ile Ser Gly Arg Ser Glu Thr Trp Leu Asn Leu Phe
                 85                  90                  95

Gly Lys Pro Asp Arg Ile Arg Thr Leu Thr Ala Gly Lys Thr Gly Arg
            100                 105                 110

Ser Arg Thr His Ser Met Ser Arg Ser Arg Asn Leu Thr Thr Thr Glu
        115                 120                 125

Gln Glu Leu Ser Arg Gln Thr Phe Leu Tyr Asp Gly Leu Gly Arg Cys
    130                 135                 140

Thr Glu Gln Arg Asp Ala Leu Gln Gln Ser Thr Leu Phe Ser Tyr Asp
145                 150                 155                 160

Asn Trp Ser Arg Met Val Ser Ser Thr Leu Ala Asp Gly Ser Val Ile
                165                 170                 175

Asn Arg Ser Tyr Ala Pro Gln Ser Ser Ser Glu Leu Ala Thr Met Leu
            180                 185                 190

Glu Val Val His Gln Asn Gly Thr Thr Arg Thr Val Ala Gly Thr Gln
        195                 200                 205

Lys Phe Asp Gly Leu Glu Arg Val Thr Gln Thr Lys Thr Gly Asp Arg
    210                 215                 220

Val Glu Gln Phe Asn Tyr Asp Ala Gly Glu Met Gln Pro Arg Ser Arg
225                 230                 235                 240

Thr Thr Ala Gly Leu Asp Asn Ile Asn Phe Thr Tyr Thr Arg Ala Leu
                245                 250                 255
```

-continued

```
Thr Asp Gln Ile Phe Ser Ser Thr Ala Pro Asp Glu Thr Ala Lys Phe
            260                 265                 270

Asp Tyr Asp Lys Thr Ser Ala Arg Leu Ile Glu Ala Thr Asn Pro Gln
        275                 280                 285

Gly Thr Arg Thr Tyr Arg Tyr Asp Val His Asn Gln Leu Thr Gly Glu
    290                 295                 300

Thr Trp Asp Asn Leu Leu Gly Gln Ala Trp Glu Thr Arg His Gln Ser
305                 310                 315                 320

Ser Leu Leu Gly Arg Pro Ile Lys Arg Thr Asp Leu Lys Lys Gly Glu
                325                 330                 335

Ala Ala Gly Ala Glu Thr Arg Tyr Asp Tyr Asp Thr Leu Gly Arg Ile
            340                 345                 350

Arg Phe Ile Asn Gln Ser Asn Leu Arg Thr Thr Ile Asp Tyr Asp Val
        355                 360                 365

Leu Gly Gln Leu Cys Lys Val Ala Thr Glu Asp Leu Gln Ala Gly Thr
    370                 375                 380

Gly Val Ile Ile Asp Met Glu Tyr Asp Asp Gln Gly Gln Glu Ile Leu
385                 390                 395                 400

Arg Thr Gln Thr Ala Ser Asn Gln Ala Ala Leu Thr Leu Thr Gln Thr
                405                 410                 415

Trp Ala Val Asp Gly Leu Leu Lys Thr Arg Asp Leu Gln Gln Ala Gly
            420                 425                 430

Ser Pro Leu Leu His Glu Thr Phe Ser Tyr Asp Pro Arg Gly Arg Leu
        435                 440                 445

Thr Leu Val Asn Tyr Leu Gly Ser Ser Leu Pro Arg Asp Glu Leu Gln
    450                 455                 460

Arg Glu Met Thr Arg Gln Ile Phe Ser Phe Asp Glu Leu Asp Asn Ile
465                 470                 475                 480

Thr Leu Cys Gln Thr Arg Phe Thr Asp Gly Thr Ser Glu Arg Ala Ala
                485                 490                 495

Phe Lys Tyr Gly Ser Pro Gly Asp Asp Lys His Lys Asp Arg Cys Gln
            500                 505                 510

Leu Leu Ser Ile Ala Tyr Thr Pro Pro Arg Lys Thr Pro Asp Pro Thr
        515                 520                 525

Phe Ser Tyr Asp Ala Asn Gly Asn Gln Leu Lys Asp Glu His Gly Asn
    530                 535                 540

Ser Leu His Tyr Asp Ser Gln Ser Arg Leu Leu Gln Val Ala Glu Thr
545                 550                 555                 560

Gly Gly Ala Pro Ile Ser Gln Tyr Arg Tyr Asp Gly His Asn Gln Leu
                565                 570                 575

Val Ala Thr Arg Asp Gly Asn Glu Ser Glu Ile Leu Arg Phe Tyr Glu
            580                 585                 590

Gly His Gln Leu Ser Ser Thr Val Gln Glu Asp Gln Arg Thr Gln Tyr
        595                 600                 605

Leu His Leu Gly Glu Gln Pro Leu Gly Gln Gln Ile Val Asp Asp Ala
    610                 615                 620

Glu Gln Thr Leu Leu Leu Leu Thr Asp Ala Asn Gln Ser Val Met Gly
625                 630                 635                 640

Glu Phe Gln Gln Gly Gln Leu Arg Lys Ala Val Tyr Ser Ala Tyr Gly
                645                 650                 655

Glu Arg His Ser Glu Glu Ala Leu Leu Ser Thr Ala Gly Phe Asn Gly
            660                 665                 670
```

-continued

```
Glu Val Arg Glu Ala Ala Asn Gly Trp Tyr Leu Leu Gly Asn Gly Tyr
        675                 680                 685

Arg Ala Tyr Asn Pro Leu Leu Met Arg Phe His Ser Pro Asp Phe Leu
    690                 695                 700

Ser Pro Phe Ala Glu Gly Gly Val Asn Pro Tyr Thr Tyr Cys Leu Gly
705                 710                 715                 720

Asn Pro Ile Ala Leu Arg Asp Pro Thr Gly His Asp Ala Ser Gly Gln
                725                 730                 735

Thr Gly Arg Leu Arg Arg Pro Asp Glu Gly Ala Leu Pro Met Gln Gln
            740                 745                 750

Gly Gly Gly Asp Ile Met Gly Trp Val Gly Val Gly Ile Gly Val Val
        755                 760                 765

Phe Thr Val Leu Gly Val Ala Ala Thr Ile Ala Thr Leu Gly Thr Ala
    770                 775                 780

Thr Pro Val Thr Gly Pro Val Thr Val Leu Gly Ile Ser Met Thr Ala
785                 790                 795                 800

Ser Ala Ala Ala Ala Val Ser Thr Val Ser Thr Gly Ala Leu Ile Val
                805                 810                 815

Gly Thr Ala Leu Thr Ala Ala Ser Thr Thr Ala Asn Thr Val Ala Ile
            820                 825                 830

Val Asn Asn Asp Gln Thr Ala Gly Glu Val Gly Gly Trp Leu Gly Ile
        835                 840                 845

Ala Ala Val Pro Val Gly Leu Val Gly Phe Gly Ala Gly Ala Val Val
    850                 855                 860

Ala Arg Ala Val Ala Ala Ala Ala Lys Val Ala Ala Ala Asn Ala Gly
865                 870                 875                 880

Thr Ile Gly Val Arg Ser Val Ser Arg Ile Gly Leu Ala Ala Ala Gly
                885                 890                 895

Ala Arg Arg Thr Ile Ser Ser Ala Ala Ser Ser Ala Arg Arg Gln Ile
            900                 905                 910

Ser Asn Met Leu Gly Arg Ile Leu Pro Arg Ala Leu Asn Arg Thr Ala
        915                 920                 925

Ala Thr Ala Arg Arg Ile Pro Ser Val Thr Ser Gly Gly Ser Gly Pro
    930                 935                 940

Gly Pro Ser Leu Phe Thr Gln Thr Thr Phe Asn Glu Ser Ile Gly Met
945                 950                 955                 960

Thr Gln Thr Thr Ile Phe Ser Thr Asn Ala Ser Gly Ile Pro Pro Ala
                965                 970                 975

Thr Gln Val Thr Arg Ile
            980
```

<210> SEQ ID NO 107
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 107

```
atgcggtgtg tgaggcgatc aagaaggttc tttaagctgc aagctgcaag ctgcaagaaa     60

aagcaggacc gctttagctt agctgacgct ccactgagta ctttccatcg aacgatccga    120

aaaaccctgc ctcgaaagct tgtcagaccc ttttctgaat cagctatcga ggtagtcatg    180

tccatcgaac cccaacgtca gaaagaacag ccacccggcc agcacacgcc agcggatcag    240

ggcccggatc gcaatgatcc ggccatcgag ccgcaggttt cggacgtaga gccggagact    300

gaaaaaggtg acggccagac gcaaggccag acccctgccc ccagccaaag ccagtcacaa    360
```

-continued

agtcagaatc agagccagca gtccaacggc agcgcttacg tgcctgacta tgagccgcag 420

gaaaaaaagg aagaccagcg caatcatcag cccactcaag gcactgatgc tgatatcgac 480

accaatgcgg gctga 495

<210> SEQ ID NO 108
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 108

Met Arg Cys Val Arg Arg Ser Arg Arg Phe Phe Lys Leu Gln Ala Ala
1 5 10 15

Ser Cys Lys Lys Lys Gln Asp Arg Phe Ser Leu Ala Asp Ala Pro Leu
20 25 30

Ser Thr Phe His Arg Thr Ile Arg Lys Thr Leu Pro Arg Lys Leu Val
35 40 45

Arg Pro Phe Ser Glu Ser Ala Ile Glu Val Val Met Ser Ile Glu Pro
50 55 60

Gln Arg Gln Lys Glu Gln Pro Pro Gly Gln His Thr Pro Ala Asp Gln
65 70 75 80

Gly Pro Asp Arg Asn Asp Pro Ala Ile Glu Pro Gln Val Ser Asp Val
85 90 95

Glu Pro Glu Thr Glu Lys Gly Asp Gly Gln Thr Gln Gly Gln Thr Pro
100 105 110

Ala Pro Ser Gln Ser Gln Ser Gln Ser Gln Asn Gln Ser Gln Gln Ser
115 120 125

Asn Gly Ser Ala Tyr Val Pro Asp Tyr Glu Pro Gln Glu Lys Lys Glu
130 135 140

Asp Gln Arg Asn His Gln Pro Thr Gln Gly Thr Asp Ala Asp Ile Asp
145 150 155 160
Thr Asn Ala Gly

<210> SEQ ID NO 109
<211> LENGTH: 702
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 109

atgcccgtca ctggtgcagg ctttatcaag cgtttgacgc aattgtccct ctgcgccggc 60

atggcgctgg tcccggtggc cgtacaggca gccgaaagcg atccttggga aggcatcaac 120

cgttccattt tcagcttcaa cgataccctt gacgcttata cgctcaagcc gctggcaaag 180

ggttatcagt acatcgctcc gcagtttgtc gaagacggta ttcataactt cttcagcaat 240

atcggcgatg tcggcaatct ggcgaacaac gtcttgcagg ccaaacctga agcggccggt 300

gtagataccg cacgccttat cgtcaacact acgttcggtc tgctgggctt cattgacgtc 360

ggcacccgca tgggcctgca acgcagtgat gaagacttcg gccagacact gggctactgg 420

ggtgtgccaa gcggcccgtt cgtggtgatt ccgctgctgg gcccaagcac ggtgcgtgac 480

gccattgcca agtacccgga cacctacacc tccccgtacc gctatattga tcacgtaccc 540

acccgcaaca cggcgttggg cgtcaatctg gtcgacacgc gtgccagcct gctgtccgcc 600

gagcgcctgg tcagtggtga tcgctacacc ttcatccgca acgcttactt gcagaaccgc 660

gaattcaagg tcaaggacgg gcaggtcgaa gacgattttt aa 702

-continued

<210> SEQ ID NO 110
<211> LENGTH: 233
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 110

Met Pro Val Thr Gly Ala Gly Phe Ile Lys Arg Leu Thr Gln Leu Ser
1 5 10 15

Leu Cys Ala Gly Met Ala Leu Val Pro Val Ala Val Gln Ala Ala Glu
20 25 30

Ser Asp Pro Trp Glu Gly Ile Asn Arg Ser Ile Phe Ser Phe Asn Asp
35 40 45

Thr Leu Asp Ala Tyr Thr Leu Lys Pro Leu Ala Lys Gly Tyr Gln Tyr
50 55 60

Ile Ala Pro Gln Phe Val Glu Asp Gly Ile His Asn Phe Phe Ser Asn
65 70 75 80

Ile Gly Asp Val Gly Asn Leu Ala Asn Asn Val Leu Gln Ala Lys Pro
85 90 95

Glu Ala Ala Gly Val Asp Thr Ala Arg Leu Ile Val Asn Thr Thr Phe
100 105 110

Gly Leu Leu Gly Phe Ile Asp Val Gly Thr Arg Met Gly Leu Gln Arg
115 120 125

Ser Asp Glu Asp Phe Gly Gln Thr Leu Gly Tyr Trp Gly Val Pro Ser
130 135 140

Gly Pro Phe Val Val Ile Pro Leu Leu Gly Pro Ser Thr Val Arg Asp
145 150 155 160

Ala Ile Ala Lys Tyr Pro Asp Thr Tyr Thr Ser Pro Tyr Arg Tyr Ile
165 170 175

Asp His Val Pro Thr Arg Asn Thr Ala Leu Gly Val Asn Leu Val Asp
180 185 190

Thr Arg Ala Ser Leu Leu Ser Ala Glu Arg Leu Val Ser Gly Asp Arg
195 200 205

Tyr Thr Phe Ile Arg Asn Ala Tyr Leu Gln Asn Arg Glu Phe Lys Val
210 215 220

Lys Asp Gly Gln Val Glu Asp Asp Phe
225 230

<210> SEQ ID NO 111
<211> LENGTH: 1194
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 111

atgacacttt caaccctgcg ccctaccccg cgccagcagt atgaatcgcc cgagtcagcc 60

gaggatttca cccagcggct ggccgacctg acccgcacgc tggccgaaac agccgagcag 120

tacgacatca gcgcgcagtt ccctcacgcc aacttccgct tgctgcacag ccacggactg 180

ctcggcctga ccgtgcctgc cgaactgggc ggcggcgctg ccgacctgtc gcgggcgcag 240

caggtcatca gcgcagtggc cagaggcgag ccttcgacag cgctgattct ggtcatgcag 300

tacctgcagc attccaggct gcaggacaac cgcaactggc cgagccacct gcgcgaacag 360

gtggccaaag acgccgtgca cgagggcgcg ctgatcaacg cgctgcgtgt cgaacccgac 420

ctgggcacac ctgcgcgtgg cggcttgccg ggcaccatcg cccggcgcag cgccgaaggc 480

tggcgcatca gcggcagcaa gatctactcc accggcagcc atggcctgac ctggttcgcc 540

-continued

gtgtgggcgc gcagcgatga cgaggacccg ctggtcggca gttggctggt gcacaaggac 600

acgcccggga tcagcatcgt cgaggactgg gaccatctgg gcatgcgcgc cacctgcagc 660

cacgaggtca ggttcgacaa cgtgcgagtg ccgctcgaac acgcggtcag cgtcagtccg 720

tggagcgccc cgcaatccga gcttgatggt gccggcatgc tgtggatgtc ggtgctgctg 780

tcgtcggtct acgatggcat cgctcaatct gcccgcgact ggctggtgca ctggctggaa 840

cagcgcacgc cttccaacct gggcgccgcg ctgtcgaccc tgccgcgctt tcaggaaaca 900

gtcgggcaga tcgacacact gctgttcgcc aaccgcagcc tgctggagtc cgccgcccaa 960

gggcacacac ccgcacagca tgccgcgcag atcaaatacc tggtgaccgg caatgccatc 1020

cgcgcagtgg aactggccat tgaggcctcg ggcaatcccg ggctttcacg cactaacccg 1080

ctgcagcgtc attaccgcaa cgtgctatgc ggccgggtgc atacgccgca gaacgacgcc 1140

gtgttgatgg gcgtgggcaa agcggtattt gcggcacgca agcagagcca gtaa 1194

<210> SEQ ID NO 112
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 112

Met Thr Leu Ser Thr Leu Arg Pro Thr Pro Arg Gln Gln Tyr Glu Ser
1 5 10 15

Pro Glu Ser Ala Glu Asp Phe Thr Gln Arg Leu Ala Asp Leu Thr Arg
20 25 30

Thr Leu Ala Glu Thr Ala Glu Gln Tyr Asp Ile Ser Ala Gln Phe Pro
35 40 45

His Ala Asn Phe Arg Leu Leu His Ser His Gly Leu Leu Gly Leu Thr
50 55 60

Val Pro Ala Glu Leu Gly Gly Gly Ala Ala Asp Leu Ser Arg Ala Gln
65 70 75 80

Gln Val Ile Ser Ala Val Ala Arg Gly Glu Pro Ser Thr Ala Leu Ile
85 90 95

Leu Val Met Gln Tyr Leu Gln His Ser Arg Leu Gln Asp Asn Arg Asn
100 105 110

Trp Pro Ser His Leu Arg Glu Gln Val Ala Lys Asp Ala Val His Glu
115 120 125

Gly Ala Leu Ile Asn Ala Leu Arg Val Glu Pro Asp Leu Gly Thr Pro
130 135 140

Ala Arg Gly Gly Leu Pro Gly Thr Ile Ala Arg Arg Ser Ala Glu Gly
145 150 155 160

Trp Arg Ile Ser Gly Ser Lys Ile Tyr Ser Thr Gly Ser His Gly Leu
165 170 175

Thr Trp Phe Ala Val Trp Ala Arg Ser Asp Asp Glu Asp Pro Leu Val
180 185 190

Gly Ser Trp Leu Val His Lys Asp Thr Pro Gly Ile Ser Ile Val Glu
195 200 205

Asp Trp Asp His Leu Gly Met Arg Ala Thr Cys Ser His Glu Val Arg
210 215 220

Phe Asp Asn Val Arg Val Pro Leu Glu His Ala Val Ser Val Ser Pro
225 230 235 240

Trp Ser Ala Pro Gln Ser Glu Leu Asp Gly Ala Gly Met Leu Trp Met
245 250 255

-continued

```
Ser Val Leu Leu Ser Ser Val Tyr Asp Gly Ile Ala Gln Ser Ala Arg
            260                 265                 270

Asp Trp Leu Val His Trp Leu Glu Gln Arg Thr Pro Ser Asn Leu Gly
        275                 280                 285

Ala Ala Leu Ser Thr Leu Pro Arg Phe Gln Glu Thr Val Gly Gln Ile
    290                 295                 300

Asp Thr Leu Leu Phe Ala Asn Arg Ser Leu Leu Glu Ser Ala Ala Gln
305                 310                 315                 320

Gly His Thr Pro Ala Gln His Ala Ala Gln Ile Lys Tyr Leu Val Thr
                325                 330                 335

Gly Asn Ala Ile Arg Ala Val Glu Leu Ala Ile Glu Ala Ser Gly Asn
            340                 345                 350

Pro Gly Leu Ser Arg Thr Asn Pro Leu Gln Arg His Tyr Arg Asn Val
        355                 360                 365

Leu Cys Gly Arg Val His Thr Pro Gln Asn Asp Ala Val Leu Met Gly
    370                 375                 380

Val Gly Lys Ala Val Phe Ala Ala Arg Lys Gln Ser Gln
385                 390                 395


<210> SEQ ID NO 113
<211> LENGTH: 882
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 113

atgaatctca caacacttcc tcttgcgctc agcattgctt gcgctgcggc catcacacct     60

gccttcgcgg gcacaagcgt ctctgaggct tcacacaaag tgaatgtgca gcaagttcgt    120

aacgcgacgg taaagatctc ctacggcggc acgacctttc tgatcgaccc gatgctggcc    180

aaaaagggaa cctacccagg gtttgaaaat acctatcgaa gcaatctgcg caatccactg    240

gttgatctga ccgaatcgcc caccgaagtg atcgccggta tcgacgcagt tatcgtcact    300

catacgcacc ttgaccattg ggacgatgct gcacaaaaag tgctgcctaa agacatccct    360

ctgttcaccc agcatgaaaa agacgcgcag ctgattcgct ctcaaggttt caagaacgta    420

cgcgtattga ctgatgaagc cgaattcggc ggcgtcaaaa ttaccaagac cggtgggcag    480

catggcaccg acgaaatgta tgccgtgcca gccctcgcga agcctctggg tgaagcaatg    540

ggcgttgtat ttcaagcccc gggctacaag accctctacc tcgctggtga cactgtctgg    600

cgtaaagagg tcgatcaggc tatcgagaac tattgtcccg aagtcatcgt actcaatgcc    660

ggcaaagcaa aaatgacggg gtatgagggg gcgatcatca tgggggaaga ggatgtactg    720

cgcgcttcac aggtcgcgaa gaacgcgaaa atcgtcgctg tacacatgaa tgcaatcaac    780

catatgtccc tgacccgtga gcaattgcgc gcttacgtca agcagcaggg tatcgaaagt    840

cgtgtagaca taccggaaga tggcgcttca ctggagttct ga                       882


<210> SEQ ID NO 114
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 114

Met Asn Leu Thr Thr Leu Pro Leu Ala Leu Ser Ile Ala Cys Ala Ala
  1               5                  10                  15

Ala Ile Thr Pro Ala Phe Ala Gly Thr Ser Val Ser Glu Ala Ser His
             20                  25                  30
```

-continued

```
Lys Val Asn Val Gln Gln Val Arg Asn Ala Thr Val Lys Ile Ser Tyr
         35                  40                  45

Gly Gly Thr Thr Phe Leu Ile Asp Pro Met Leu Ala Lys Lys Gly Thr
     50                  55                  60

Tyr Pro Gly Phe Glu Asn Thr Tyr Arg Ser Asn Leu Arg Asn Pro Leu
 65                  70                  75                  80

Val Asp Leu Thr Glu Ser Pro Thr Glu Val Ile Ala Gly Ile Asp Ala
                 85                  90                  95

Val Ile Val Thr His Thr His Leu Asp His Trp Asp Asp Ala Ala Gln
            100                 105                 110

Lys Val Leu Pro Lys Asp Ile Pro Leu Phe Thr Gln His Glu Lys Asp
        115                 120                 125

Ala Gln Leu Ile Arg Ser Gln Gly Phe Lys Asn Val Arg Val Leu Thr
    130                 135                 140

Asp Glu Ala Glu Phe Gly Gly Val Lys Ile Thr Lys Thr Gly Gly Gln
145                 150                 155                 160

His Gly Thr Asp Glu Met Tyr Ala Val Pro Ala Leu Ala Lys Pro Leu
                165                 170                 175

Gly Glu Ala Met Gly Val Val Phe Gln Ala Pro Gly Tyr Lys Thr Leu
            180                 185                 190

Tyr Leu Ala Gly Asp Thr Val Trp Arg Lys Glu Val Asp Gln Ala Ile
        195                 200                 205

Glu Asn Tyr Cys Pro Glu Val Ile Val Leu Asn Ala Gly Lys Ala Lys
    210                 215                 220

Met Thr Gly Tyr Glu Gly Ala Ile Ile Met Gly Glu Glu Asp Val Leu
225                 230                 235                 240

Arg Ala Ser Gln Val Ala Lys Asn Ala Lys Ile Val Ala Val His Met
                245                 250                 255

Asn Ala Ile Asn His Met Ser Leu Thr Arg Glu Gln Leu Arg Ala Tyr
            260                 265                 270

Val Lys Gln Gln Gly Ile Glu Ser Arg Val Asp Ile Pro Glu Asp Gly
        275                 280                 285

Ala Ser Leu Glu Phe
    290
```

<210> SEQ ID NO 115
<211> LENGTH: 2379
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 115

```
atgcatctgt tgccgtttgc gcgttacccc ttatcacctg cagaaacacc taaacccaag     60

gtgaccatga aggttggaga tttcagggct tacgacaccg ctccagcacc cggagtgacc    120

actgcgtcct gcggacaact ggcaatcggc accaagttag aaatcatcga gaccgccgag    180

aatggcgaac ttacttatgc caagggtaag attctatctg gcagcgtgaa gcaggggca     240

accaaaaaac gggtcgaggg ggcggaggtc tggttcgctt atttgaaaaa cggcgaaccc    300

tacaaaaact cagtccctaa gcgcatctgg ctcgctgacg atgtgcctga gcgagcaaga    360

cccaattact ggcagggtaa ggtcaaagcc tcagtagtga ataagttgcc gctgtacgat    420

gatcctgcca gccctacaaa tggccagcct gcaggcgccc ggaaggggac tctggagctg    480

gtcatgaaca gcgtcatcga gtttaactct tcggaagtcg tcaacctggc gctggatggc    540

aagctgcatc ggatggccaa gtgcacgatg ctgagtggcg gcctgcgggg tcatggtgcg    600
```

-continued

gttcccccca gcttttgggc atgtgttgaa aatgaccctg ctaataaagt attgaaatgg 660

gactcggtaa cgccgaccag ttttgatacg gtcgttatga cgagcaccgg agtgaaggcg 720

ggcgatccaa ttggctatct tggacaaacc gaaaatctca ccggtgaaaa tggcggcgtc 780

agcagcaaat accaggttca cgtcgaaatt ttcacagccg atgctgaggt taaagacttc 840

ctcaagaaca ccgcgggttt gaagattggg aagcaatacc tgcaccttgc aagcggggct 900

gtactcaagc aaaaagcgcc cgcgaccggc accacagcac tcaagcaaga ccatgcggtt 960

gacttggcta aagccacaat tgtcaaagaa ggcaccgatg actggtatga ggtcagcgtg 1020

atcgaggacg atcagcctgt agccggcctg ataaaaaaag ccactgcgct agtcatcaca 1080

cagcacgatt gggaaaaatt gggctttcag atcgtagagg agaacaacgc agcagccgat 1140

ggtttcttgg acccggatgc aatgccacag ttcttcaaag acctattcgc gaagatcgac 1200

aagaaccacg atggtgaggt ggagcctgct gaactggctg aggctcttaa gaaaccggaa 1260

accagaaccc agtgggccag gcttgttgcc catcacccta cggagtggaa agataaggca 1320

ggctccccca agtggagcaa gttggataaa ctgctggaaa cgtcgccgaa gatgttgaaa 1380

catgaaaaag aacgcattga taaatatgta ttttgggatg agttgtcagg gaaagctaag 1440

atgacctcaa gtttaatatg gcattttcat ccggtagaat tcatttcaac atttagcgca 1500

aaaaaagtct gcgcttgcaa cgccatagtt aaggctactc gctgggtttc ttccagtaag 1560

acgcactatg gcccattgca tacgggtgat aaagagcttg ggagtgcacc tcagtgggat 1620

gacctggtct cagaaggaaa aataacggaa gaggagaaaa aaattattgt tgtaatgtct 1680

ggaaacgagg caaaaattaa cggagtacaa agttatgata gcgaaataat tactgccggc 1740

gcgatgcaga aaacaattaa cttgtccggt ggcggtgagc tgccactaca agttaagaag 1800

tttaaaaatc agcatcccga ggcgtacatc gaatactttg attctcaagg ctggaagttg 1860

gatgagacag gtgattcggc gaaaatgtat tatcaagggc cggctcgagc tagtggcgca 1920

aagctggaag gaaaggcgct gaaggataat ttaaaaattg gttgcagtga atcgacattt 1980

gggaaggtgg ttgactgtca acctgtttca gtgatggcct gcgctatcgc aagtccgtta 2040

tatatccaga tacaaataat ggattttata gaaaggttac gtagttcttt aacgaagaag 2100

cccacaggct ataactttac tgctgggga tttttcaaga cctctctcgg aaaagctgtg 2160

gttttggatc acgatataaa tcgacccggg tatgtgaagg atgacttggg atctgctctt 2220

gacacttttt ttgctcaaaa tccaacagtc agccgggata ttgatacatg gggcgcagca 2280

tatagcgtta atgagcgaaa agttttagac ctgtatggcg ctcgaagaag aatgaccaat 2340

gcattgcttc gatacaatca cttgaaggcg gagttataa 2379

<210> SEQ ID NO 116
<211> LENGTH: 792
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 116

Met His Leu Leu Pro Phe Ala Arg Tyr Pro Leu Ser Pro Ala Glu Thr
1 5 10 15

Pro Lys Pro Lys Val Thr Met Lys Val Gly Asp Phe Arg Ala Tyr Asp
20 25 30

Thr Ala Pro Ala Pro Gly Val Thr Thr Ala Ser Cys Gly Gln Leu Ala
35 40 45

Ile Gly Thr Lys Leu Glu Ile Ile Glu Thr Ala Glu Asn Gly Glu Leu
50 55 60

-continued

```
Thr Tyr Ala Lys Gly Lys Ile Leu Ser Gly Ser Val Lys Gln Gly Ala
 65                  70                  75                  80

Thr Lys Lys Arg Val Glu Gly Ala Glu Val Trp Phe Ala Tyr Leu Lys
                 85                  90                  95

Asn Gly Glu Pro Tyr Lys Asn Ser Val Pro Lys Arg Ile Trp Leu Ala
            100                 105                 110

Asp Asp Val Pro Glu Arg Ala Arg Pro Asn Tyr Trp Gln Gly Lys Val
        115                 120                 125

Lys Ala Ser Val Val Asn Lys Leu Pro Leu Tyr Asp Asp Pro Ala Ser
    130                 135                 140

Pro Thr Asn Gly Gln Pro Ala Gly Ala Arg Lys Gly Thr Leu Glu Leu
145                 150                 155                 160

Val Met Asn Ser Val Ile Glu Phe Asn Ser Ser Glu Val Val Asn Leu
                165                 170                 175

Ala Leu Asp Gly Lys Leu His Arg Met Ala Lys Cys Thr Met Leu Ser
            180                 185                 190

Gly Gly Leu Arg Gly His Gly Ala Val Pro Pro Ser Phe Trp Ala Cys
        195                 200                 205

Val Glu Asn Asp Pro Ala Asn Lys Val Leu Lys Trp Asp Ser Val Thr
    210                 215                 220

Pro Thr Ser Phe Asp Thr Val Val Met Thr Ser Thr Gly Val Lys Ala
225                 230                 235                 240

Gly Asp Pro Ile Gly Tyr Leu Gly Gln Thr Glu Asn Leu Thr Gly Glu
                245                 250                 255

Asn Gly Gly Val Ser Ser Lys Tyr Gln Val His Val Glu Ile Phe Thr
            260                 265                 270

Ala Asp Ala Glu Val Lys Asp Phe Leu Lys Asn Thr Ala Gly Leu Lys
        275                 280                 285

Ile Gly Lys Gln Tyr Leu His Leu Ala Ser Gly Ala Val Leu Lys Gln
    290                 295                 300

Lys Ala Pro Ala Thr Gly Thr Thr Ala Leu Lys Gln Asp His Ala Val
305                 310                 315                 320

Asp Leu Ala Lys Ala Thr Ile Val Lys Glu Gly Thr Asp Asp Trp Tyr
                325                 330                 335

Glu Val Ser Val Ile Glu Asp Asp Gln Pro Val Ala Gly Leu Ile Lys
            340                 345                 350

Lys Ala Thr Ala Leu Val Ile Thr Gln His Asp Trp Glu Lys Leu Gly
        355                 360                 365

Phe Gln Ile Val Glu Glu Asn Asn Ala Ala Ala Asp Gly Phe Leu Asp
    370                 375                 380

Pro Asp Ala Met Pro Gln Phe Phe Lys Asp Leu Phe Ala Lys Ile Asp
385                 390                 395                 400

Lys Asn His Asp Gly Glu Val Glu Pro Ala Glu Leu Ala Glu Ala Leu
                405                 410                 415

Lys Lys Pro Glu Thr Arg Thr Gln Trp Ala Arg Leu Val Ala His His
            420                 425                 430

Pro Thr Glu Trp Lys Asp Lys Ala Gly Ser Pro Lys Trp Ser Lys Leu
        435                 440                 445

Asp Lys Leu Leu Glu Thr Ser Pro Lys Met Leu Lys His Glu Lys Glu
    450                 455                 460

Arg Ile Asp Lys Tyr Val Phe Trp Asp Glu Leu Ser Gly Lys Ala Lys
465                 470                 475                 480
```

-continued

```
Met Thr Ser Ser Leu Ile Trp His Phe His Pro Val Glu Phe Ile Ser
                485                 490                 495

Thr Phe Ser Ala Lys Lys Val Cys Ala Cys Asn Ala Ile Val Lys Ala
            500                 505                 510

Thr Arg Trp Val Ser Ser Ser Lys Thr His Tyr Gly Pro Leu His Thr
        515                 520                 525

Gly Asp Lys Glu Leu Gly Ser Ala Pro Gln Trp Asp Asp Leu Val Ser
    530                 535                 540

Glu Gly Lys Ile Thr Glu Glu Glu Lys Lys Ile Ile Val Val Met Ser
545                 550                 555                 560

Gly Asn Glu Ala Lys Ile Asn Gly Val Gln Ser Tyr Asp Ser Glu Ile
                565                 570                 575

Ile Thr Ala Gly Ala Met Gln Lys Thr Ile Asn Leu Ser Gly Gly Gly
            580                 585                 590

Glu Leu Pro Leu Gln Val Lys Lys Phe Lys Asn Gln His Pro Glu Ala
        595                 600                 605

Tyr Ile Glu Tyr Phe Asp Ser Gln Gly Trp Lys Leu Asp Glu Thr Gly
    610                 615                 620

Asp Ser Ala Lys Met Tyr Tyr Gln Gly Pro Ala Arg Ala Ser Gly Ala
625                 630                 635                 640

Lys Leu Glu Gly Lys Ala Leu Lys Asp Asn Leu Lys Ile Gly Cys Ser
                645                 650                 655

Glu Ser Thr Phe Gly Lys Val Val Asp Cys Gln Pro Val Ser Val Met
            660                 665                 670

Ala Cys Ala Ile Ala Ser Pro Leu Tyr Ile Gln Ile Gln Ile Met Asp
        675                 680                 685

Phe Ile Glu Arg Leu Arg Ser Ser Leu Thr Lys Lys Pro Thr Gly Tyr
    690                 695                 700

Asn Phe Thr Ala Gly Gly Phe Phe Lys Thr Ser Leu Gly Lys Ala Val
705                 710                 715                 720

Val Leu Asp His Asp Ile Asn Arg Pro Gly Tyr Val Lys Asp Asp Leu
                725                 730                 735

Gly Ser Ala Leu Asp Thr Phe Phe Ala Gln Asn Pro Thr Val Ser Arg
            740                 745                 750

Asp Ile Asp Thr Trp Gly Ala Ala Tyr Ser Val Asn Glu Arg Lys Val
        755                 760                 765

Leu Asp Leu Tyr Gly Ala Arg Arg Arg Met Thr Asn Ala Leu Leu Arg
    770                 775                 780

Tyr Asn His Leu Lys Ala Glu Leu
785                 790


<210> SEQ ID NO 117
<211> LENGTH: 1554
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 117

atgcggccgt tgcctgcgtt cagtattttg cagtttgatc cgttgaaacg ttcgggtcct     60

gcgctgacgg tcgaacgtga tacaccggtc gatagcaagc ctattaatga cgtgcgttgt    120

cgcttccgta cgtgctaccc gaccgaagtt caggcgctgg atctgaccgc gctgaattac    180

tcggtgaaag gcggtggttc gttgctcagc ctgcgcctgg agatgagcgc tgaaggtcac    240

ttgggtgagc ttgaactgag ccgcctgcgt ctgcactttg caggcgagcg ctatatcagc    300

cagatgctgt acctctgcct gctacgcaat ctcgagggta tcgagctgat ccctctggac    360
```

-continued

```
gctgccggca agcccatcga cggtgtcaat ggcgcgccaa tggcgttcaa gatgccgggc    420

gaccgtgtac agccggtagg gtttgccgaa gaagaggcgt tgatcccgta tccgctgaac    480

acgttccgcg gttatcgcta cctgcaggag tacttcgcgt ttcaggacaa gttcctgttc    540

gtcgacatca acggtctgga tctgctcaac gcactgccag aagagacact caaacaagtg    600

cgcggccttg agttgcgctt tgatattcgc aagagcggca ttcagcgtct tcgtcccacc    660

ctggataacg taaagctgta ttgcacgccg atcgtcaact tgttcaagca cgacgccttg    720

ccgattcgcc ttgatggcaa gcaggacgag tacctgctgc tgcccgccga atatggcctg    780

gaaacctgtg gtgtgttttc ggttgaaacc gtgaccggtt ggaagccggg aggtcttggc    840

tatcaggatt atgtgccgtt cgaatccttt gagcacgacc ccagtttcga cgtgcccaac    900

agccgtccgc attacagcat tcgccagcgt tcttctttgc tccatgaagg cctcgacact    960

tatctgagtt tcggcattcg ccatacagaa gcgcacgaaa ccctgtcgat cgagttgatg   1020

tgcaccaatc agaacctgcc acgcaaactc aaactgggcg aaatcaacgt ggcctgcgaa   1080

gatacgccgg agtttttgag tttccgcaat atcacaccgg ctacctccag tttcgcgccc   1140

ccgctgaacc gtgacttcct gtggaagttg atcagcaata tgtcgctcaa ttacttgtct   1200

ctggctgacg tcaatgcgct gaaggtgatt ctggaaacct acgatttgcc ccgttactac   1260

gaccagcacg cggaaaaagt cagcaagcgc ctgttgggcg gtttgaaatc gatcaagcat   1320

caacacgtgg acagattgca ccgagggtta ccggtacgcg gattgcgcac tgagctgacc   1380

atcgacccgg aagggtatat cggcgaaggc gacatgtttg tattcgcttc ggttctcaac   1440

gagtttttcg cgctttacgc cagtctcaat tcgtaccacg agctgcgggt aaaaagcaca   1500

cagggagagg tgtaccaatg gacaccacgt atgggcctcc agcccctgct ttaa         1554
```

<210> SEQ ID NO 118
<211> LENGTH: 517
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 118

```
Met Arg Pro Leu Pro Ala Phe Ser Ile Leu Gln Phe Asp Pro Leu Lys
  1               5                  10                  15

Arg Ser Gly Pro Ala Leu Thr Val Glu Arg Asp Thr Pro Val Asp Ser
             20                  25                  30

Lys Pro Ile Asn Asp Val Arg Cys Arg Phe Arg Thr Cys Tyr Pro Thr
         35                  40                  45

Glu Val Gln Ala Leu Asp Leu Thr Ala Leu Asn Tyr Ser Val Lys Gly
     50                  55                  60

Gly Gly Ser Leu Leu Ser Leu Arg Leu Glu Met Ser Ala Glu Gly His
 65                  70                  75                  80

Leu Gly Glu Leu Glu Leu Ser Arg Leu Arg Leu His Phe Ala Gly Glu
                 85                  90                  95

Arg Tyr Ile Ser Gln Met Leu Tyr Leu Cys Leu Leu Arg Asn Leu Glu
            100                 105                 110

Gly Ile Glu Leu Ile Pro Leu Asp Ala Ala Gly Lys Pro Ile Asp Gly
        115                 120                 125

Val Asn Gly Ala Pro Met Ala Phe Lys Met Pro Gly Asp Arg Val Gln
    130                 135                 140

Pro Val Gly Phe Ala Glu Glu Glu Ala Leu Ile Pro Tyr Pro Leu Asn
145                 150                 155                 160
```

-continued

```
Thr Phe Arg Gly Tyr Arg Tyr Leu Gln Glu Tyr Phe Ala Phe Gln Asp
                165                 170                 175

Lys Phe Leu Phe Val Asp Ile Asn Gly Leu Asp Leu Leu Asn Ala Leu
            180                 185                 190

Pro Glu Glu Thr Leu Lys Gln Val Arg Gly Leu Glu Leu Arg Phe Asp
        195                 200                 205

Ile Arg Lys Ser Gly Ile Gln Arg Leu Arg Pro Thr Leu Asp Asn Val
    210                 215                 220

Lys Leu Tyr Cys Thr Pro Ile Val Asn Leu Phe Lys His Asp Ala Leu
225                 230                 235                 240

Pro Ile Arg Leu Asp Gly Lys Gln Asp Glu Tyr Leu Leu Leu Pro Ala
                245                 250                 255

Glu Tyr Gly Leu Glu Thr Cys Gly Val Phe Ser Val Glu Thr Val Thr
            260                 265                 270

Gly Trp Lys Pro Gly Gly Leu Gly Tyr Gln Asp Tyr Val Pro Phe Glu
        275                 280                 285

Ser Phe Glu His Asp Pro Ser Phe Asp Val Pro Asn Ser Arg Pro His
    290                 295                 300

Tyr Ser Ile Arg Gln Arg Ser Ser Leu Leu His Glu Gly Leu Asp Thr
305                 310                 315                 320

Tyr Leu Ser Phe Gly Ile Arg His Thr Glu Ala His Glu Thr Leu Ser
                325                 330                 335

Ile Glu Leu Met Cys Thr Asn Gln Asn Leu Pro Arg Lys Leu Lys Leu
            340                 345                 350

Gly Glu Ile Asn Val Ala Cys Glu Asp Thr Pro Glu Phe Leu Ser Phe
        355                 360                 365

Arg Asn Ile Thr Pro Ala Thr Ser Ser Phe Ala Pro Pro Leu Asn Arg
    370                 375                 380

Asp Phe Leu Trp Lys Leu Ile Ser Asn Met Ser Leu Asn Tyr Leu Ser
385                 390                 395                 400

Leu Ala Asp Val Asn Ala Leu Lys Val Ile Leu Glu Thr Tyr Asp Leu
                405                 410                 415

Pro Arg Tyr Tyr Asp Gln His Ala Glu Lys Val Ser Lys Arg Leu Leu
            420                 425                 430

Gly Gly Leu Lys Ser Ile Lys His Gln His Val Asp Arg Leu His Arg
        435                 440                 445

Gly Leu Pro Val Arg Gly Leu Arg Thr Glu Leu Thr Ile Asp Pro Glu
    450                 455                 460

Gly Tyr Ile Gly Glu Gly Asp Met Phe Val Phe Ala Ser Val Leu Asn
465                 470                 475                 480

Glu Phe Phe Ala Leu Tyr Ala Ser Leu Asn Ser Tyr His Glu Leu Arg
                485                 490                 495

Val Lys Ser Thr Gln Gly Glu Val Tyr Gln Trp Thr Pro Arg Met Gly
            500                 505                 510

Leu Gln Pro Leu Leu
        515
```

<210> SEQ ID NO 119
<211> LENGTH: 5874
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

-continued

<400> SEQUENCE: 119

atggtcaagg ttacctcttc cggatttact gccaaccctc tctctcatca tgcggacagt 60

gtttcccccg cgaacagtcc ccctcagtta ccggagcctg tgcatctggt tgatttaagc 120

gagtcgtccc gcaagggcgg catgcgaaat cggccgcatg ccagtttgaa cagtcaggtg 180

ctcgaactgc aagcggtgcc gtcgcaacgt ggaaagcatg ttcgtgtcag aagtcatgcc 240

gatggcgaga gtgtcattaa tgcctggctg gcaaagcgcc cctcggttca aagcgaaacc 300

agtcttgata acgatggcaa actggtgcgt tacacccccg tgaatcatga gccgctggcg 360

ccgcgcaatg aggcgttttt cacctcggtg ccggggatgt tgatggccgt tttgacggtc 420

caccccgaga tggaacatgg catcagcggg gacataactg ctgatgctgt ggctgcccgg 480

cttgccgaac cgccaatagg gttgctaacc ggaatctggc agtcttccca tgatcgagcc 540

tatctggagc gtggcggtgt ggtgcatacc gccaatatgg aagagcgctg ggcgccgttg 600

acgctgccag gcatcaatcc ccgagagccc ctgcgaatgg ccggtttgca ggccgatggt 660

ggagtctatc tgcataacgg cagccaactg tggcgcttga ccgaaactgc cgccgagtcc 720

gtgaccaccg aaaaccttcc tgaaggtgcg gcggtacgca ttggcgccgg tggcgaggtg 780

catgggctgc atgaaggcgc gcttcattcg aatggcattt cccgtccaat cgagctttgg 840

cggccaaaag ctggcgcgcc ggggcgcgag cagagtccgg cgcgccccgt tgatttgctg 900

ccgttaccgg gtggcaccgc tgcactgatc cttgatgaca agggacgtat ttatcacgct 960

gatctgaaag gcacaggcgc tgttgaagcc caccggctga aattacctgc tgactttgcg 1020

cagggtaaag gttgggccgt gaccgccatg ggattgtccc gagacgacac tgttcatctg 1080

atgctgcagg atcagaacgg gcgtcgcatg agcttgcagc gagcaccggg cgaggcgctg 1140

tttcgtcctg cgtacctgct ggatcgcccg ttgctgctgc tctataccga agggctgcat 1200

gttccgtcgg aggccgcggt gcagtcgcac gttcagcttg atggtcatgc tcaactgggg 1260

catatcgatg gcgtgctgca ttataaagcg gctcccgatc agtcatggga acggctaaag 1320

cagtcgggcg gcgaaccgct gacgggtttg actgctcttt attccagccc gctgggattt 1380

atcgacagga aaccggtttt cgctttagtg ggggatgccc ggcaggtggt cgagttgaaa 1440

ctggaggggc gtacatcctg gttgccgagc gatgccgagc ttccgcgtca ccctgcgggc 1500

gggcctttgg cggtgatacc ggatacggta gcgttacgca ccagcccgat cgcgcagttt 1560

gacgagcctg tacaggcgct ggcggttcac ggtaatcgcc gggtcgtcgc gctgacggat 1620

tcggggcgat taatggctgc cgatgcggac accccagccc gccgacttcc cacgttgcag 1680

cgccccatcg ccatcgccgt agggctcaac gatcagttac tggtgctgca tcatccccat 1740

agccagcgcc cccagttgaa acggttgagt gcgaaagatg actgggagcc ggtgccgata 1800

attctgccgg gtattgttca cccttcaagt cttcgcgcta ctcgcacggg gcaaatacaa 1860

gtgcagctgg gagaaaactg gcatacgttg ctgccatcaa tgacgtcgca cgataatcag 1920

cgcttacctg cccgcgtaaa acctgaacca gaggggggatg aggcgccgtc ggcgaatttc 1980

ctggcgggta gcaacgccct cgccaatcag cagcaagcca gtcgtatcag cacaccgcat 2040

catgacgcat cggtggttac gacgctggcg gggacaacag ccaacaaccc gttgacgatg 2100

gcgtcgagcc tacaggcagt ggttgatacg acccgcgctc aggtaggcgc gttggcgaga 2160

gatgtagtgg gcgcagcggc gaacagcacg atgcgggcaa tggcgcatac cttgggtgtt 2220

gtactgccgc caacgcctca ggagaagcgc ctggccagtt tccataatga ggcgaaacag 2280

gcttatacat caggaaaaat actgtttgag catctgccgt cactcgcgca agtgcgcgtc 2340

-continued

```
gcttcagccg tagggccgtc ggacggagaa agattcgggc tgtcacatca gcaaacgcaa   2400

cgcttgttga cgctgcgaga ggggaagctg gaagcgctgt tacgcgactt gcgcaagatc   2460

ggctttcatg aaggggtgat catgggcgat atgggcgaca gcgacagtgc gcacggtctt   2520

gtttcgacga catcgacacc aacgttccgg ctggccgagc tatggcgacg gcagcattcg   2580

cgagtggata aggcgctgtc ttccgctgga ttatccagat cggaagatat ttttccggac   2640

ttgaacctaa gtatcaacgc gttggctggc ggcgcggcgc tgaatgcgga tcgtatgagc   2700

gaacgtgaag ctgagttgtt gagcgttttg tgcgaggtca gcgaaaaaat gatgcgcgct   2760

ggcgtacgct tgccggcaga tgatggaagc gttgacagcg cccacagcca ggcgccatac   2820

ggcttgagaa cagcaggatt gattgcaggt ctggtggact atgatgcgct gttgagcagt   2880

accgacgcgc aggcgctgga aatggcggag cgacttcagc aagatgccag gcttgctgca   2940

ttgtgcaaac tcggtctgtc ttcgtggggt caattagcgg ccttcgatga tgtggtgacg   3000

acgtttcgcg aacagatatc gttaccgggc tcggcacgcc gcacccagtt gctcaaaaat   3060

cttggcttgc cacccgatgc cgcgccggac gaaatggcgg cgcgcatgtc cgacttactc   3120

ctggatctgt tcaaccggag caccttcttt tcgacgcagt cgcgtggtct ggaactgcgc   3180

ggttcgttgg gatcggctga ctggaaacat ctcaatgcgt tcagcgtcgg cgtgactggc   3240

gaggcgcttc aagtgctcgg cgtagagcgc atcggcgatg gcaaggacgg cgatgccggg   3300

ttggtcgcgt tttttgtgcg ccacgccaaa gcctctgtat ctgcgacgtc agggatcgga   3360

atcgatttca agccaggccc cggcactggc ggccgtgtta ttgattcgcg accgggtcgc   3420

tcgatgaact cgacgtgggg aggctctacc aacctgggta tttccggcgc gtaccagcat   3480

ggtcagggcg ccgccgtgat catcgcaccg tcgacgatct ccgatttcgt gcggctgtta   3540

ttcgatgtca accatcccga taccacccaa atcctgcgca ccggtgtgaa cggtggttcg   3600

attggtcttg atctgtttga aaccaatgtg aatgcctctg tgggggcgaa cgtcagcgta   3660

tcgccattca gcctgagcca gaaatatggg ccacagaaac cgacggcaga tgcggccgtc   3720

tctggcccag acaatcggcg cagcaccgcg tcagggtcgt tgtcggtagg cgggacggct   3780

caggctggcg cgcactgggg gcaaatggag ttgcacctgg atcacgcctg ggccgatatt   3840

atcggtctgg aatttcaggg ccgcacggat ttcaatcttg aattcaatag cggcctgaat   3900

ctgggaggcg cgctgtcttc cgcgctgggc gataaccccc aaaagttgat aaatgcgtcc   3960

actggaaacg gcaatctgca actcgccggc atccgcgtcg cgtcaagcga tgtgcagttg   4020

ccgaccgatg ctgtggttga cgacaagcgc cgtggccccct tcctgtcgac ggccagctat   4080

aaacgcacct tcgataccga agttgccaag cctgttacgg ccggggagtg gagccagatg   4140

cgccagcgcc ttgccaaagc ctttcctgac aatatcgcag agttgggcgc gctcgattac   4200

cccaccaggc ccggtgagcg tatcgcgacc atcaaacagg tgattgaccg catacaaggt   4260

gcgaaggcgc gtagcgtgga agccgtcggt gcaatggacg gaaaggcatt gcaccgtcag   4320

cgtttcgatg ccgcgagaga aatgtcgaac gccggcaaca gcgtatggcg ggcgagttcc   4380

gaaattgagc gcgcctcgat cgtggagatg ctgcatcagt tgcgtcagca ggaacaaagc   4440

gccgtccaga atcacgcccg agccattccc ggcgcgcgtg tggaattcaa cctgttcggt   4500

cgtgaatcgc tggaaacggt ggtctttcac gccatcggtc atctggggct tggcagcaag   4560

ctgaacgatc tggcggagct gcgtcgcaag gtgccgggtc tcgatcaggt catgctgagt   4620

ttccagtcgt tgcccaaggt caatcaggtg cgctacgttt ttgagatgcg ccctcaggcg   4680

aggttcgcca tcaatgacgc gctactggcg cgcgagcagc aggcatcggc acgtgcgctc   4740
```

-continued

```
ggtttgcagg gaccctcggg aagtgaattg aattggcgcg gcgttctgga caagatcaaa   4800

accacgcctg acctttatcg gctggcggcg atcgccgtac ataacaccga tgaaaacccc   4860

gtgacctcaa gaatagggct gccgctgctg aatgtgtcgg ccacaggcgc gacatcgcat   4920

cagttgttcg aggcggaaat ccagttccga tacggtctgt atgacggtct gcaaggggtt   4980

gagttgctgg aggccggaaa cagggcattg cagtcgccgt tacgggcatt acagcaatcc   5040

ggtattcagg ccctggggca gagaacccag gccggggagg ttgcgtatgg ccccccttcg   5100

ccgcgcaaag agtcgccgtt gcgcaccgca gtggatgctg ctgcgctgac aacgagtgac   5160

atcgcgcgac aacttgaggt taaagtccag cgcatgaata ccgcgcatga gcgtgaggcg   5220

aatgctatca gttcgttcca gcaggcttat gggatcgcgt ccgcgcatct agacaggctg   5280

cttttgcgca ttcctgaatt gccattacct gaaattgatg accgcgacgt cgatggagga   5340

cgtgtgcgcg gtacatttgc gtcgctccag cgacatcatc aggcgctgga tgacgctata   5400

agtgccatgc atcaggccag cgaaaaggtg tacacgatac ctggcaagca ggccactcaa   5460

gagcaagacc cggcgctggc tcaactgctc tctgttgaaa aacgtcggcg ttcgctcggg   5520

catgccttgg aaacactggc gggcagaggg gtggaagcgg gcacggccac agggcttgaa   5580

cttaacaggg tctcatcgca agtgaatgat ctggtcgctc gccgggacgc gctgctaagg   5640

cagcgtgaaa gcggtgttca ggagggcggt ctggatagcg aagagctgga aatggaactt   5700

caattgacca cctcagtgct gcagcggttg cgcgccgatt tgctcggcga gcggcaggcg   5760

atggaggcta ccgccaaacg cctggatcag gcgagccgcg ctgccctcga aggtgagcgc   5820

agcttcagcg acgccgtgcg tgacagggcg tggggcgaac tcgataacgt gtag         5874
```

<210> SEQ ID NO 120
<211> LENGTH: 1957
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 120

```
Met Val Lys Val Thr Ser Ser Gly Phe Thr Ala Asn Pro Leu Ser His
  1               5                  10                  15

His Ala Asp Ser Val Ser Pro Ala Asn Ser Pro Pro Gln Leu Pro Glu
             20                  25                  30

Pro Val His Leu Val Asp Leu Ser Glu Ser Ser Arg Lys Gly Gly Met
         35                  40                  45

Arg Asn Arg Pro His Ala Ser Leu Asn Ser Gln Val Leu Glu Leu Gln
     50                  55                  60

Ala Val Pro Ser Gln Arg Gly Lys His Val Arg Val Arg Ser His Ala
 65                  70                  75                  80

Asp Gly Glu Ser Val Ile Asn Ala Trp Leu Ala Lys Arg Pro Ser Val
                 85                  90                  95

Gln Ser Glu Thr Ser Leu Asp Asn Asp Gly Lys Leu Val Arg Tyr Thr
            100                 105                 110

Pro Val Asn His Glu Pro Leu Ala Pro Arg Asn Glu Ala Phe Phe Thr
        115                 120                 125

Ser Val Pro Gly Met Leu Met Ala Val Leu Thr Val His Pro Glu Met
    130                 135                 140

Glu His Gly Ile Ser Gly Asp Ile Thr Ala Asp Ala Val Ala Ala Arg
145                 150                 155                 160

Leu Ala Glu Pro Pro Ile Gly Leu Leu Thr Gly Ile Trp Gln Ser Ser
                165                 170                 175
```

-continued

```
His Asp Arg Ala Tyr Leu Glu Arg Gly Gly Val Val His Thr Ala Asn
            180                 185                 190

Met Glu Glu Arg Trp Ala Pro Leu Thr Leu Pro Gly Ile Asn Pro Arg
        195                 200                 205

Glu Pro Leu Arg Met Ala Gly Leu Gln Ala Asp Gly Gly Val Tyr Leu
    210                 215                 220

His Asn Gly Ser Gln Leu Trp Arg Leu Thr Glu Thr Ala Ala Glu Ser
225                 230                 235                 240

Val Thr Thr Glu Asn Leu Pro Glu Gly Ala Ala Val Arg Ile Gly Ala
                245                 250                 255

Gly Gly Glu Val His Gly Leu His Glu Gly Ala Leu His Ser Asn Gly
            260                 265                 270

Ile Ser Arg Pro Ile Glu Leu Trp Arg Pro Lys Ala Gly Ala Pro Gly
        275                 280                 285

Arg Glu Gln Ser Pro Ala Arg Pro Val Asp Leu Leu Pro Leu Pro Gly
    290                 295                 300

Gly Thr Ala Ala Leu Ile Leu Asp Asp Lys Gly Arg Ile Tyr His Ala
305                 310                 315                 320

Asp Leu Lys Gly Thr Gly Ala Val Glu Ala His Arg Leu Lys Leu Pro
                325                 330                 335

Ala Asp Phe Ala Gln Gly Lys Gly Trp Ala Val Thr Ala Met Gly Leu
            340                 345                 350

Ser Arg Asp Asp Thr Val His Leu Met Leu Gln Asp Gln Asn Gly Arg
        355                 360                 365

Arg Met Ser Leu Gln Arg Ala Pro Gly Glu Ala Leu Phe Arg Pro Ala
    370                 375                 380

Tyr Leu Leu Asp Arg Pro Leu Leu Leu Leu Tyr Thr Glu Gly Leu His
385                 390                 395                 400

Val Pro Ser Glu Ala Ala Val Gln Ser His Val Gln Leu Asp Gly His
                405                 410                 415

Ala Gln Leu Gly His Ile Asp Gly Val Leu His Tyr Lys Ala Ala Pro
            420                 425                 430

Asp Gln Ser Trp Glu Arg Leu Lys Gln Ser Gly Gly Glu Pro Leu Thr
        435                 440                 445

Gly Leu Thr Ala Leu Tyr Ser Ser Pro Leu Gly Phe Ile Asp Arg Lys
    450                 455                 460

Pro Val Phe Ala Leu Val Gly Asp Ala Arg Gln Val Val Glu Leu Lys
465                 470                 475                 480

Leu Glu Gly Arg Thr Ser Trp Leu Pro Ser Asp Ala Glu Leu Pro Arg
                485                 490                 495

His Pro Ala Gly Gly Pro Leu Ala Val Ile Pro Asp Thr Val Ala Leu
            500                 505                 510

Arg Thr Ser Pro Ile Ala Gln Phe Asp Glu Pro Val Gln Ala Leu Ala
        515                 520                 525

Val His Gly Asn Arg Arg Val Val Ala Leu Thr Asp Ser Gly Arg Leu
    530                 535                 540

Met Ala Ala Asp Ala Asp Thr Pro Ala Arg Arg Leu Pro Thr Leu Gln
545                 550                 555                 560

Arg Pro Ile Ala Ile Ala Val Gly Leu Asn Asp Gln Leu Leu Val Leu
                565                 570                 575

His His Pro His Ser Gln Arg Pro Gln Leu Lys Arg Leu Ser Ala Lys
            580                 585                 590
```

-continued

```
Asp Asp Trp Glu Pro Val Pro Ile Ile Leu Pro Gly Ile Val His Pro
        595                 600                 605

Ser Ser Leu Arg Ala Thr Arg Thr Gly Gln Ile Gln Val Gln Leu Gly
    610                 615                 620

Glu Asn Trp His Thr Leu Leu Pro Ser Met Thr Ser His Asp Asn Gln
625                 630                 635                 640

Arg Leu Pro Ala Arg Val Lys Pro Glu Pro Glu Gly Asp Glu Ala Pro
                645                 650                 655

Ser Ala Asn Phe Leu Ala Gly Ser Asn Ala Leu Ala Asn Gln Gln Gln
            660                 665                 670

Ala Ser Arg Ile Ser Thr Pro His His Asp Ala Ser Val Val Thr Thr
        675                 680                 685

Leu Ala Gly Thr Thr Ala Asn Asn Pro Leu Thr Met Ala Ser Ser Leu
    690                 695                 700

Gln Ala Val Val Asp Thr Thr Arg Ala Gln Val Gly Ala Leu Ala Arg
705                 710                 715                 720

Asp Val Val Gly Ala Ala Ala Asn Ser Thr Met Arg Ala Met Ala His
                725                 730                 735

Thr Leu Gly Val Val Leu Pro Pro Thr Pro Gln Glu Lys Arg Leu Ala
            740                 745                 750

Ser Phe His Asn Glu Ala Lys Gln Ala Tyr Thr Ser Gly Lys Ile Leu
        755                 760                 765

Phe Glu His Leu Pro Ser Leu Ala Gln Val Arg Val Ala Ser Ala Val
    770                 775                 780

Gly Pro Ser Asp Gly Glu Arg Phe Gly Leu Ser His Gln Gln Thr Gln
785                 790                 795                 800

Arg Leu Leu Thr Leu Arg Glu Gly Lys Leu Glu Ala Leu Leu Arg Asp
                805                 810                 815

Leu Arg Lys Ile Gly Phe His Glu Gly Val Ile Met Gly Asp Met Gly
            820                 825                 830

Asp Ser Asp Ser Ala His Gly Leu Val Ser Thr Thr Ser Thr Pro Thr
        835                 840                 845

Phe Arg Leu Ala Glu Leu Trp Arg Arg Gln His Ser Arg Val Asp Lys
    850                 855                 860

Ala Leu Ser Ser Ala Gly Leu Ser Arg Ser Glu Asp Ile Phe Pro Asp
865                 870                 875                 880

Leu Asn Leu Ser Ile Asn Ala Leu Ala Gly Gly Ala Ala Leu Asn Ala
                885                 890                 895

Asp Arg Met Ser Glu Arg Glu Ala Glu Leu Leu Ser Val Leu Cys Glu
            900                 905                 910

Val Ser Glu Lys Met Met Arg Ala Gly Val Arg Leu Pro Ala Asp Asp
        915                 920                 925

Gly Ser Val Asp Ser Ala His Ser Gln Ala Pro Tyr Gly Leu Arg Thr
    930                 935                 940

Ala Gly Leu Ile Ala Gly Leu Val Asp Tyr Asp Ala Leu Leu Ser Ser
945                 950                 955                 960

Thr Asp Ala Gln Ala Leu Glu Met Ala Glu Arg Leu Gln Gln Asp Ala
                965                 970                 975

Arg Leu Ala Ala Leu Cys Lys Leu Gly Leu Ser Ser Trp Gly Gln Leu
            980                 985                 990

Ala Ala Phe Asp Asp Val Val Thr Thr Phe Arg Glu Gln Ile Ser Leu
        995                1000                1005
```

-continued

```
Pro Gly Ser Ala Arg Arg Thr Gln Leu Leu Lys Asn Leu Gly Leu Pro
   1010                1015                1020

Pro Asp Ala Ala Pro Asp Glu Met Ala Ala Arg Met Ser Asp Leu Leu
1025                1030                1035                1040

Leu Asp Leu Phe Asn Arg Ser Thr Phe Phe Ser Thr Gln Ser Arg Gly
                1045                1050                1055

Leu Glu Leu Arg Gly Ser Leu Gly Ser Ala Asp Trp Lys His Leu Asn
            1060                1065                1070

Ala Phe Ser Val Gly Val Thr Gly Glu Ala Leu Gln Val Leu Gly Val
        1075                1080                1085

Glu Arg Ile Gly Asp Gly Lys Asp Gly Asp Ala Gly Leu Val Ala Phe
    1090                1095                1100

Phe Val Arg His Ala Lys Ala Ser Val Ser Ala Thr Ser Gly Ile Gly
1105                1110                1115                1120

Ile Asp Phe Lys Pro Gly Pro Gly Thr Gly Gly Arg Val Ile Asp Ser
                1125                1130                1135

Arg Pro Gly Arg Ser Met Asn Ser Thr Trp Gly Gly Ser Thr Asn Leu
            1140                1145                1150

Gly Ile Ser Gly Ala Tyr Gln His Gly Gln Gly Ala Ala Val Ile Ile
        1155                1160                1165

Ala Pro Ser Thr Ile Ser Asp Phe Val Arg Leu Leu Phe Asp Val Asn
    1170                1175                1180

His Pro Asp Thr Thr Gln Ile Leu Arg Thr Gly Val Asn Gly Gly Ser
1185                1190                1195                1200

Ile Gly Leu Asp Leu Phe Glu Thr Asn Val Asn Ala Ser Val Gly Ala
                1205                1210                1215

Asn Val Ser Val Ser Pro Phe Ser Leu Ser Gln Lys Tyr Gly Pro Gln
            1220                1225                1230

Lys Pro Thr Ala Asp Ala Ala Val Ser Gly Pro Asp Asn Arg Arg Ser
        1235                1240                1245

Thr Ala Ser Gly Ser Leu Ser Val Gly Gly Thr Ala Gln Ala Gly Ala
    1250                1255                1260

His Trp Gly Gln Met Glu Leu His Leu Asp His Ala Trp Ala Asp Ile
1265                1270                1275                1280

Ile Gly Leu Glu Phe Gln Gly Arg Thr Asp Phe Asn Leu Glu Phe Asn
                1285                1290                1295

Ser Gly Leu Asn Leu Gly Gly Ala Leu Ser Ser Ala Leu Gly Asp Asn
            1300                1305                1310

Pro Gln Lys Leu Ile Asn Ala Ser Thr Gly Asn Gly Asn Leu Gln Leu
        1315                1320                1325

Ala Gly Ile Arg Val Ala Ser Ser Asp Val Gln Leu Pro Thr Asp Ala
    1330                1335                1340

Val Val Asp Asp Lys Arg Arg Gly Pro Phe Leu Ser Thr Ala Ser Tyr
1345                1350                1355                1360

Lys Arg Thr Phe Asp Thr Glu Val Ala Lys Pro Val Thr Ala Gly Glu
                1365                1370                1375

Trp Ser Gln Met Arg Gln Arg Leu Ala Lys Ala Phe Pro Asp Asn Ile
            1380                1385                1390

Ala Glu Leu Gly Ala Leu Asp Tyr Pro Thr Arg Pro Gly Glu Arg Ile
        1395                1400                1405

Ala Thr Ile Lys Gln Val Ile Asp Arg Ile Gln Gly Ala Lys Ala Arg
    1410                1415                1420
```

-continued

```
Ser Val Glu Ala Val Gly Ala Met Asp Gly Lys Ala Leu His Arg Gln
1425               1430                1435                1440

Arg Phe Asp Ala Ala Arg Glu Met Ser Asn Ala Gly Asn Ser Val Trp
             1445                1450                1455

Arg Ala Ser Ser Glu Ile Glu Arg Ala Ser Ile Val Glu Met Leu His
          1460                1465                1470

Gln Leu Arg Gln Gln Glu Gln Ser Ala Val Gln Asn His Ala Arg Ala
       1475                1480                1485

Ile Pro Gly Ala Arg Val Glu Phe Asn Leu Phe Gly Arg Glu Ser Leu
   1490                1495                1500

Glu Thr Val Val Phe His Ala Ile Gly His Leu Gly Leu Gly Ser Lys
1505               1510                1515                1520

Leu Asn Asp Leu Ala Glu Leu Arg Arg Lys Val Pro Gly Leu Asp Gln
             1525                1530                1535

Val Met Leu Ser Phe Gln Ser Leu Pro Lys Val Asn Gln Val Arg Tyr
          1540                1545                1550

Val Phe Glu Met Arg Pro Gln Ala Arg Phe Ala Ile Asn Asp Ala Leu
       1555                1560                1565

Leu Ala Arg Glu Gln Gln Ala Ser Ala Arg Ala Leu Gly Leu Gln Gly
   1570                1575                1580

Pro Ser Gly Ser Glu Leu Asn Trp Arg Gly Val Leu Asp Lys Ile Lys
1585               1590                1595                1600

Thr Thr Pro Asp Leu Tyr Arg Leu Ala Ala Ile Ala Val His Asn Thr
             1605                1610                1615

Asp Glu Asn Pro Val Thr Ser Arg Ile Gly Leu Pro Leu Leu Asn Val
          1620                1625                1630

Ser Ala Thr Gly Ala Thr Ser His Gln Leu Phe Glu Ala Glu Ile Gln
       1635                1640                1645

Phe Arg Tyr Gly Leu Tyr Asp Gly Leu Gln Gly Val Glu Leu Leu Glu
   1650                1655                1660

Ala Gly Asn Arg Ala Leu Gln Ser Pro Leu Arg Ala Leu Gln Gln Ser
1665               1670                1675                1680

Gly Ile Gln Ala Leu Gly Gln Arg Thr Gln Ala Gly Glu Val Ala Tyr
             1685                1690                1695

Gly Pro Pro Ser Pro Arg Lys Glu Ser Pro Leu Arg Thr Ala Val Asp
          1700                1705                1710

Ala Ala Ala Leu Thr Thr Ser Asp Ile Ala Arg Gln Leu Glu Val Lys
       1715                1720                1725

Val Gln Arg Met Asn Thr Ala His Glu Arg Glu Ala Asn Ala Ile Ser
   1730                1735                1740

Ser Phe Gln Gln Ala Tyr Gly Ile Ala Ser Ala His Leu Asp Arg Leu
1745               1750                1755                1760

Leu Leu Arg Ile Pro Glu Leu Pro Leu Pro Glu Ile Asp Asp Arg Asp
             1765                1770                1775

Val Asp Gly Gly Arg Val Arg Gly Thr Phe Ala Ser Leu Gln Arg His
          1780                1785                1790

His Gln Ala Leu Asp Asp Ala Ile Ser Ala Met His Gln Ala Ser Glu
       1795                1800                1805

Lys Val Tyr Thr Ile Pro Gly Lys Gln Ala Thr Gln Glu Gln Asp Pro
   1810                1815                1820

Ala Leu Ala Gln Leu Leu Ser Val Glu Lys Arg Arg Arg Ser Leu Gly
1825               1830                1835                1840
```

-continued

```
His Ala Leu Glu Thr Leu Ala Gly Arg Gly Val Glu Ala Gly Thr Ala
               1845                1850                1855

Thr Gly Leu Glu Leu Asn Arg Val Ser Ser Gln Val Asn Asp Leu Val
           1860                1865                1870

Ala Arg Arg Asp Ala Leu Leu Arg Gln Arg Glu Ser Gly Val Gln Glu
       1875                1880                1885

Gly Gly Leu Asp Ser Glu Glu Leu Glu Met Glu Leu Gln Leu Thr Thr
   1890                1895                1900

Ser Val Leu Gln Arg Leu Arg Ala Asp Leu Leu Gly Glu Arg Gln Ala
1905               1910                1915                1920

Met Glu Ala Thr Ala Lys Arg Leu Asp Gln Ala Ser Arg Ala Ala Leu
               1925                1930                1935

Glu Gly Glu Arg Ser Phe Ser Asp Ala Val Arg Asp Arg Ala Trp Gly
           1940                1945                1950

Glu Leu Asp Asn Val
       1955
```

<210> SEQ ID NO 121
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 121

```
atgaacatta cgccgctcac gtcagccgcg ggcaagggct cgtccgcaca aggcacagac     60

aaaatttcca ttcccaactc cacgcgcatg atcaatgccg cttcaatcaa gtggttgaat    120

aaggtgcgta gcgccatcag tgaccacatc cgcaccagca tcgagaaagg gaaactgttc    180

gagctcgcct ccttgggcag caacatgttc ggtgtcccgg ctctttcagc gcgcccctcg    240

acgctccaac ctgtgttggc gtttgaggct gaccccaatc acgacctgaa ccttgtcagg    300

gtctatatgc aggacagcgc cggcaagctc actccctggg acccgacgcc caacgcggtc    360

acgacgacgt cgaatccatc agagcctgat gcgcagagcg atacggcttc gtcatcatta    420

cctcggcggc ctcccgcagg ctcggtgctg agtttgctgg gcattgcgct ggatcacgcg    480

caacgccaca gtcctcgcgc ggacaggtct gccaagggac gacctggccg agaggagagg    540

aacggggcaa ggttcaatgc caagcaaaca aagccgacag aggctgaagc ctacggtgat    600

catcagacac ccaatcctga tttgcacagg caaaaagaga cagctcaacg cgttgctgaa    660

agcatcaaca gcatgcgaga gcagcaaaat ggaatgcaac gcgccgaagg gcttctcaga    720

gccaaagaag cgttgcaagc tcgggaagcc gcgcgcaagc agcttctgga cgtgctcgag    780

gccatccagg ctggccgtga agactccacc gacaagaaga tcagcgccac tgaaaagaac    840

gccacgggca tcaactacca gtga                                           864
```

<210> SEQ ID NO 122
<211> LENGTH: 287
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 122

```
Met Asn Ile Thr Pro Leu Thr Ser Ala Ala Gly Lys Gly Ser Ser Ala
  1               5                  10                  15

Gln Gly Thr Asp Lys Ile Ser Ile Pro Asn Ser Thr Arg Met Ile Asn
             20                  25                  30

Ala Ala Ser Ile Lys Trp Leu Asn Lys Val Arg Ser Ala Ile Ser Asp
         35                  40                  45
```

-continued

```
His Ile Arg Thr Ser Ile Glu Lys Gly Lys Leu Phe Glu Leu Ala Ser
     50                  55                  60

Leu Gly Ser Asn Met Phe Gly Val Pro Ala Leu Ser Ala Arg Pro Ser
 65                  70                  75                  80

Thr Leu Gln Pro Val Leu Ala Phe Glu Ala Asp Pro Asn His Asp Leu
                85                  90                  95

Asn Leu Val Arg Val Tyr Met Gln Asp Ser Ala Gly Lys Leu Thr Pro
            100                 105                 110

Trp Asp Pro Thr Pro Asn Ala Val Thr Thr Thr Ser Asn Pro Ser Glu
        115                 120                 125

Pro Asp Ala Gln Ser Asp Thr Ala Ser Ser Ser Leu Pro Arg Arg Pro
    130                 135                 140

Pro Ala Gly Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Asp His Ala
145                 150                 155                 160

Gln Arg His Ser Pro Arg Ala Asp Arg Ser Ala Lys Gly Arg Pro Gly
                165                 170                 175

Arg Glu Glu Arg Asn Gly Ala Arg Phe Asn Ala Lys Gln Thr Lys Pro
            180                 185                 190

Thr Glu Ala Glu Ala Tyr Gly Asp His Gln Thr Pro Asn Pro Asp Leu
        195                 200                 205

His Arg Gln Lys Glu Thr Ala Gln Arg Val Ala Glu Ser Ile Asn Ser
    210                 215                 220

Met Arg Glu Gln Gln Asn Gly Met Gln Arg Ala Glu Gly Leu Leu Arg
225                 230                 235                 240

Ala Lys Glu Ala Leu Gln Ala Arg Glu Ala Ala Arg Lys Gln Leu Leu
                245                 250                 255

Asp Val Leu Glu Ala Ile Gln Ala Gly Arg Glu Asp Ser Thr Asp Lys
            260                 265                 270

Lys Ile Ser Ala Thr Glu Lys Asn Ala Thr Gly Ile Asn Tyr Gln
        275                 280                 285


<210> SEQ ID NO 123
<211> LENGTH: 837
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 123

atgaccttaa gaatcaatac tcgttctgct accccggttg tacctctgga aacaggctct     60

acatcgcagc cgacaccacc gccggtcacg gcaagagcga ctgagcctcc ccccgtcgcc    120

aatcctgcgg cgcctaaatc agcgccaggt gttcagcaag cacacgggct gaagacgcgc    180

atcgctggca agctttccga acgtcagacc aatttcagtc tcgggattcc cggcactggt    240

cgtactctca accggccctt gcgcagcggg attccggagg aaggtgagca ggtatcgaac    300

gaggagagtc atgatccgtt gctcaaggaa gcgcatgaac tgcagcgtat ggtggagtcg    360

gcgctgaccc atctgaaggc ggcaccgacg tctctctggg agcgtcccgc cccttcaacg    420

gtaaggcgta ttaccaccaa gatttttccg tggctaaagc ctgccccgct gcgcgaagtc    480

gcaagcaatg gcagcaacgc caagaccaag atcaagatca actcacagca aagccctgaa    540

accatcgcag cggcggtgaa agagctgagc acccggctcg atcaccagag caaggtgctc    600

gccacagcca cccacgcact ggtcgctgcg cgtgagcatc ttgaatcgct cgaacaggcc    660

accccgccct cgtcgaccga accactggac catgccaggg ctcgcgttca acaagccgac    720
```

-continued

tccaccaccc gcctggccag tcagcaactt cgtgagctga ttcagggtac agacgtgttg 780

caactgggcg cgctgagtga agggcaggat caggttgaac agaaagccga gttttct 837

<210> SEQ ID NO 124
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 124

Met Thr Leu Arg Ile Asn Thr Arg Ser Ala Thr Pro Val Val Pro Leu
1 5 10 15

Glu Thr Gly Ser Thr Ser Gln Pro Thr Pro Pro Pro Val Thr Ala Arg
20 25 30

Ala Thr Glu Pro Pro Pro Val Ala Asn Pro Ala Ala Pro Lys Ser Ala
35 40 45

Pro Gly Val Gln Gln Ala His Gly Leu Lys Thr Arg Ile Ala Gly Lys
50 55 60

Leu Ser Glu Arg Gln Thr Asn Phe Ser Leu Gly Ile Pro Gly Thr Gly
65 70 75 80

Arg Thr Leu Asn Arg Pro Leu Arg Ser Gly Ile Pro Glu Glu Gly Glu
85 90 95

Gln Val Ser Asn Glu Glu Ser His Asp Pro Leu Leu Lys Glu Ala His
100 105 110

Glu Leu Gln Arg Met Val Glu Ser Ala Leu Thr His Leu Lys Ala Ala
115 120 125

Pro Thr Ser Leu Trp Glu Arg Pro Ala Pro Ser Thr Val Arg Arg Ile
130 135 140

Thr Thr Lys Ile Phe Pro Trp Leu Lys Pro Ala Pro Leu Arg Glu Val
145 150 155 160

Ala Ser Asn Gly Ser Asn Ala Lys Thr Lys Ile Lys Ile Asn Ser Gln
165 170 175

Gln Ser Pro Glu Thr Ile Ala Ala Ala Val Lys Glu Leu Ser Thr Arg
180 185 190

Leu Asp His Gln Ser Lys Val Leu Ala Thr Ala Thr His Ala Leu Val
195 200 205

Ala Ala Arg Glu His Leu Glu Ser Leu Glu Gln Ala Thr Pro Pro Ser
210 215 220

Ser Thr Glu Pro Leu Asp His Ala Arg Ala Arg Val Gln Gln Ala Asp
225 230 235 240

Ser Thr Thr Arg Leu Ala Ser Gln Gln Leu Arg Glu Leu Ile Gln Gly
245 250 255

Thr Asp Val Leu Gln Leu Gly Ala Leu Ser Glu Gly Gln Asp Gln Val
260 265 270

Glu Gln Lys Ala Glu Phe Ser
275

<210> SEQ ID NO 125
<211> LENGTH: 615
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 125

ataggtaata tttgcggcac ctcgggctca cgtcatgtgt atagcccatc ccatacacaa 60

cgaataactt cagctccctc tacatccact catgttggtg gagatacact gacatccatt 120

catcagcttt cgcatagtca gagagagcag tttctgaaca tgcatgatcc aatgagagta 180

-continued

atgggacttg accatgatac cgagcttttc agaacgacgg atagtcgcta tataaaaaac 240

gataaactcg cgggcaatcc acaatccatg gcgagtatcc ttatgcatga agaactgcgc 300

cccaatcgtt ttgccagcca tacaggtgcc caaccacacg aagcaagggc gtacgttccg 360

aaaagaataa aagccaccga tctaggagtt ccatcactga acgtaatgac tggctcgcta 420

gcgcgagacg gaattagagc ttatgatcac atgagtgata atcaggtctc tgtcaaaatg 480

cgactgggag attttctcga aaggggtggc aaggtctatg ccgacgcttc gtctgtagct 540

gacgatgggg aaacatcaca agctctgatt gtcacattgc ccaaaggaca gaaagtgccg 600

gtcgaaaggg tctga 615

<210> SEQ ID NO 126
<211> LENGTH: 204
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 126

Met Gly Asn Ile Cys Gly Thr Ser Gly Ser Arg His Val Tyr Ser Pro
1 5 10 15

Ser His Thr Gln Arg Ile Thr Ser Ala Pro Ser Thr Ser Thr His Val
20 25 30

Gly Gly Asp Thr Leu Thr Ser Ile His Gln Leu Ser His Ser Gln Arg
35 40 45

Glu Gln Phe Leu Asn Met His Asp Pro Met Arg Val Met Gly Leu Asp
50 55 60

His Asp Thr Glu Leu Phe Arg Thr Thr Asp Ser Arg Tyr Ile Lys Asn
65 70 75 80

Asp Lys Leu Ala Gly Asn Pro Gln Ser Met Ala Ser Ile Leu Met His
85 90 95

Glu Glu Leu Arg Pro Asn Arg Phe Ala Ser His Thr Gly Ala Gln Pro
100 105 110

His Glu Ala Arg Ala Tyr Val Pro Lys Arg Ile Lys Ala Thr Asp Leu
115 120 125

Gly Val Pro Ser Leu Asn Val Met Thr Gly Ser Leu Ala Arg Asp Gly
130 135 140

Ile Arg Ala Tyr Asp His Met Ser Asp Asn Gln Val Ser Val Lys Met
145 150 155 160

Arg Leu Gly Asp Phe Leu Glu Arg Gly Gly Lys Val Tyr Ala Asp Ala
165 170 175

Ser Ser Val Ala Asp Asp Gly Glu Thr Ser Gln Ala Leu Ile Val Thr
180 185 190

Leu Pro Lys Gly Gln Lys Val Pro Val Glu Arg Val
195 200

<210> SEQ ID NO 127
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: HIV TAT domain

-continued

<400> SEQUENCE: 127

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> SEQ ID NO 128
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 128

agtaggatcc atagaaaaat accatagggg tgca 34

<210> SEQ ID NO 129
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 129

agtatctaga tcacttgtca tcgtcgtcct tgtagtcgtc aatcacatgc gcttg 55

<210> SEQ ID NO 130
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 130

atgcggatcc cgtatgacct tgtaaaat 28

<210> SEQ ID NO 131
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 131

atgctctaga tcaagcgtaa tctggaacat cgtatgggta gccgttgtaa aactgctt 58

<210> SEQ ID NO 132
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 132

agtcggatcc gataatcctg gatgatccat tg 32

<210> SEQ ID NO 133
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 133

agtcctcgag tcacttgtca tcgtcgtcct tgtagtcttg atgtgccctg tactt 55

-continued

<210> SEQ ID NO 134
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 134

agtaaagctt acgggcaggt attgcaag 28

<210> SEQ ID NO 135
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 135

agtatctaga tcacttgtca tcgtcgtcct tgtagtcttt tttgggcagc cagcg 55

<210> SEQ ID NO 136
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 136

agtaggatcc tgcctccaac tattggct 28

<210> SEQ ID NO 137
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 137

agtatctaga tcacttgtca tcgtcgtcct tgtagtctct cgctttgaac gcctg 55

<210> SEQ ID NO 138
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 138

ataggatccc gagaacggcg cggacgtg 28

<210> SEQ ID NO 139
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 139

atatctagat catttatcat catcatcttt ataatcctcg tcagagctct ctgc 54

<210> SEQ ID NO 140
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 140

gatggatcca cgcacataac aacggtg 27

<210> SEQ ID NO 141
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 141

atatctagat catttatcat catcatcttt ataatcaatc tgacttaata c 51

<210> SEQ ID NO 142
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 142

attggtacct ctagaggatc caaccttcaa tctgaa 36

<210> SEQ ID NO 143
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 143

atgtcgactt agcggtagag cattgcg 27

<210> SEQ ID NO 144
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 144

gcgaattcgt tagttgattt tgtctagcg 29

<210> SEQ ID NO 145
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 145

gaggatccgc cgttgtaaaa ctgcttaga 29

<210> SEQ ID NO 146
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 146

gtaaaacgac ggccagt 17

-continued

<210> SEQ ID NO 147
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 147

atgagaattc gcatctccat gcatctt 27

<210> SEQ ID NO 148
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 148

cggactcgag ctcagggcgc gaaactga 28

<210> SEQ ID NO 149
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 149

gtatggtacc ccgacctggc aaccgcag 28

<210> SEQ ID NO 150
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 150

agtcctcgag actaaagagg gtatacgaat gggaaatata 40

<210> SEQ ID NO 151
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 151

agtcgatatc tcattgccag ttacggtacg ggc 33

<210> SEQ ID NO 152
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 152

gatggatcca agtaaccggt ctgcaca 27

<210> SEQ ID NO 153
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 153

atatctagat catttatcat catcatcttt atatgacttt tgagccgcct g 51

<210> SEQ ID NO 154
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 154

ggcctcgaga tggacgggtc cggggagcag ctt 33

<210> SEQ ID NO 155
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 155

ggcactagtt cagcccatct tcttccagat ggtg 34

<210> SEQ ID NO 156
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 156

cacctattta attcgttgag aaacaatgaa aata 34

<210> SEQ ID NO 157
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 157

gacatctcgt ctcgccaagc c 21

<210> SEQ ID NO 158
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 158

caccaagcaa cgtctggagg caacaatgca 30

<210> SEQ ID NO 159
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 159

gtcgcctagg aaattattta gttcccatga 30

-continued

<210> SEQ ID NO 160
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 160

caccaagatc ggagaggatc agaatatggc g 31

<210> SEQ ID NO 161
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 161

ggggactatt ctaaaagcat acttggc 27

<210> SEQ ID NO 162
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 162

caccttagcg taaggagcta acaatgaacc c 31

<210> SEQ ID NO 163
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 163

gtttcgcgcc ctgagcgc 18

<210> SEQ ID NO 164
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 164

cacccatagg ggtgcaataa caatgaatag a 31

<210> SEQ ID NO 165
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 165

gtcaatcaca tgcgcttggc c 21

<210> SEQ ID NO 166
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 166

aaaaagcagg cttcgaagga gatagaacca tgtatagccc atcc 44

<210> SEQ ID NO 167
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 167

agaaagctgg gtaacagacc ctttcgac 28

<210> SEQ ID NO 168
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 168

cacccacata ggatatgtaa acaatgcaaa taaagaac 38

<210> SEQ ID NO 169
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 169

gccgttgtaa aactgcttag aggc 24

<210> SEQ ID NO 170
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 170

caccacaaag aggttttcaa acaatgaatc 30

<210> SEQ ID NO 171
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 171

gcagtagagc gtgtcgcgac 20

<210> SEQ ID NO 172
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 172

atacataacg ctggccta 18

-continued

<210> SEQ ID NO 173
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 173

cggatccatg acaatcgt 18

<210> SEQ ID NO 174
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 174

gcaaatcctt taagctct 18

<210> SEQ ID NO 175
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 175

tgtttcgcta agccactg 18

<210> SEQ ID NO 176
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 176

tcgcgccaaa ccagggag 18

<210> SEQ ID NO 177
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 177

tcccacattc tgcaacgc 18

<210> SEQ ID NO 178
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 178

aaccccattc agtcacgc 18

<210> SEQ ID NO 179
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 179

tttgccatgc gtgattgc 18

<210> SEQ ID NO 180
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 180

cctctacgat ctattcaa 18

<210> SEQ ID NO 181
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 181

ggcaatgctc gcggcctg 18

<210> SEQ ID NO 182
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 182

tccggtagct cgtcagcg 18

<210> SEQ ID NO 183
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 183

gtggatgacc acatagttat g 21

<210> SEQ ID NO 184
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 184

agcccatccc atacacaa 18

<210> SEQ ID NO 185
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 185

cactttctgt cctttggg 18

-continued

<210> SEQ ID NO 186
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 186

tattcagctt caagaatg 18

<210> SEQ ID NO 187
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 187

acccgcatag acctgtctg 19

<210> SEQ ID NO 188
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 188

atcactccgt ctcgatatc 19

<210> SEQ ID NO 189
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 189

tgccctgtac ttcatgcg 18

<210> SEQ ID NO 190
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 190

ctatgtattt caaaacac 18

<210> SEQ ID NO 191
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 191

atcaccctct gtaattccc 19

<210> SEQ ID NO 192
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 192

cgcatttcaa ccagctca 18

<210> SEQ ID NO 193
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 193

cagcaccgga agcccttc 18

<210> SEQ ID NO 194
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 194

ggtaatattt gtggtacttc 20

<210> SEQ ID NO 195
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 195

cagatgtaac gtgacatc 18

<210> SEQ ID NO 196
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 196

acagtcagca atcactcg 18

<210> SEQ ID NO 197
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 197

tacactccat acactgctg 19

<210> SEQ ID NO 198
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 198

ttgaattcat gaaaatacat aacgctgg 28

-continued

<210> SEQ ID NO 199
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 199

ttctcgagtc agacatctcg tctcgc 26

<210> SEQ ID NO 200
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 200

ttggatccgt atgcacgcaa atcctttaag ctc 33

<210> SEQ ID NO 201
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 201

ttctcgagtc agtcgcctag gaaattattt agttcc 36

<210> SEQ ID NO 202
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 202

ttgaattcat gaatagagtt tccggtagct c 31

<210> SEQ ID NO 203
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 203

ttctcgagtc agtcaatcac atgcgcttgg 30

<210> SEQ ID NO 204
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 204

ttgaattcat gggtaatatt tgcggcacct c 31

<210> SEQ ID NO 205
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

-continued

<400> SEQUENCE: 205

ttctcgagtc agacccttтc gaccgg 26

<210> SEQ ID NO 206
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 206

ttgaattcat gcaaataaag aacagtcatc tc 32

<210> SEQ ID NO 207
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 207

ttctcgagtc agccgttgta aaactgctta gag 33

<210> SEQ ID NO 208
<211> LENGTH: 1185
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 208

atgactgcct acgatgtaga aaaggaatgg agcagaattt ccaatactgc cgctaaaact 60

caccagaaca acgattttga aggtttcacc taccaggact tcagaaccca cgtaccgatc 120

atggacaagg aaggcttcgc ggcacaaacc gaacgctgcc ttgagcgcaa cgagcgcaac 180

tgcctgatcg gctttaccag tggcaccagc ggcaacctca aacgctgtta ttactactac 240

gactgtgaag tcgatgaaga cagttcccgc tccaacgtct tccgcagcaa tggtttcatt 300

caacccggtg atcgctgcgc caacctgttc accatcaacc tgttttctgc cctgaacaac 360

atcaccacca tgatggccgg taactgcggt gcgcatgtgg tgtccgtagg cgatatcacc 420

ctgctgacca agagtcactt cgaggcgctc aactcgatca agctcaacgt actgctcggc 480

gtaccctcga ccatcctgca gttcatcgat gccatgcagc agcacggtgt gcacatcgat 540

atcgaaaagg tcgtcttcaa tggcgagggc ctgaaaacct ttcagaagaa aatcatcagg 600

gaagcctttg gcgaacaggt ctccatcgtc ggcgtatatg gcagttccga gggcggcatt 660

ctgggtttca ccaacagccc ttgccacacc gaatacgagt ttctttccga caaatacttc 720

atcgagaaag aaggcgacag catcctcatc acctcgttga cccgcgagaa cttcacaccg 780

ctgctccggt atcgcctggg agacaccgca acgctttcgc tgaaaggcga caagctctat 840

ttgactgaca tccagcggga ggacatgagc ttcaacttca tgggcaacct cattggtctg 900

ggcatcattc aacaagcgat caaacagaca ctgggccgca cgctggaaat ccaggttcac 960

ctgtcagtga ctgatgcgcg caaagaactg gtgaccgttt tcgttcaggc ctcggaagtc 1020

aacgaagatg aacgcgccag aatcgaaaca gccatcgccg atattccgga catcaacgag 1080

gcctatcaga aagaccaggg cagcgtgctg gttgtgcgca aggatgccag agactacgcc 1140

gtctcggagc gaggcaaaat gctctacatc attgaccgca ggaat 1185

-continued

<210> SEQ ID NO 209
<211> LENGTH: 395
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas syringae pv. tomato DC3000

<400> SEQUENCE: 209

Met Thr Ala Tyr Asp Val Glu Lys Glu Trp Ser Arg Ile Ser Asn Thr
1 5 10 15

Ala Ala Lys Thr His Gln Asn Asn Asp Phe Glu Gly Phe Thr Tyr Gln
20 25 30

Asp Phe Arg Thr His Val Pro Ile Met Asp Lys Glu Gly Phe Ala Ala
35 40 45

Gln Thr Glu Arg Cys Leu Glu Arg Asn Glu Arg Asn Cys Leu Ile Gly
50 55 60

Phe Thr Ser Gly Thr Ser Gly Asn Leu Lys Arg Cys Tyr Tyr Tyr Tyr
65 70 75 80

Asp Cys Glu Val Asp Glu Asp Ser Ser Arg Ser Asn Val Phe Arg Ser
85 90 95

Asn Gly Phe Ile Gln Pro Gly Asp Arg Cys Ala Asn Leu Phe Thr Ile
100 105 110

Asn Leu Phe Ser Ala Leu Asn Asn Ile Thr Thr Met Met Ala Gly Asn
115 120 125

Cys Gly Ala His Val Val Ser Val Gly Asp Ile Thr Leu Leu Thr Lys
130 135 140

Ser His Phe Glu Ala Leu Asn Ser Ile Lys Leu Asn Val Leu Leu Gly
145 150 155 160

Val Pro Ser Thr Ile Leu Gln Phe Ile Asp Ala Met Gln Gln His Gly
165 170 175

Val His Ile Asp Ile Glu Lys Val Val Phe Asn Gly Glu Gly Leu Lys
180 185 190

Thr Phe Gln Lys Lys Ile Ile Arg Glu Ala Phe Gly Glu Gln Val Ser
195 200 205

Ile Val Gly Val Tyr Gly Ser Ser Glu Gly Gly Ile Leu Gly Phe Thr
210 215 220

Asn Ser Pro Cys His Thr Glu Tyr Glu Phe Leu Ser Asp Lys Tyr Phe
225 230 235 240

Ile Glu Lys Glu Gly Asp Ser Ile Leu Ile Thr Ser Leu Thr Arg Glu
245 250 255

Asn Phe Thr Pro Leu Leu Arg Tyr Arg Leu Gly Asp Thr Ala Thr Leu
260 265 270

Ser Leu Lys Gly Asp Lys Leu Tyr Leu Thr Asp Ile Gln Arg Glu Asp
275 280 285

Met Ser Phe Asn Phe Met Gly Asn Leu Ile Gly Leu Gly Ile Ile Gln
290 295 300

Gln Ala Ile Lys Gln Thr Leu Gly Arg Thr Leu Glu Ile Gln Val His
305 310 315 320

Leu Ser Val Thr Asp Ala Arg Lys Glu Leu Val Thr Val Phe Val Gln
325 330 335

Ala Ser Glu Val Asn Glu Asp Glu Arg Ala Arg Ile Glu Thr Ala Ile
340 345 350

Ala Asp Ile Pro Asp Ile Asn Glu Ala Tyr Gln Lys Asp Gln Gly Ser
355 360 365

-continued

```
Val Leu Val Val Arg Lys Asp Ala Arg Asp Tyr Ala Val Ser Glu Arg
    370                 375                 380

Gly Lys Met Leu Tyr Ile Ile Asp Arg Arg Asn
385                 390                 395
```

What is claimed:

1. A method of modifying a cell death pathway in a cell comprising:

introducing into a cell (i) a protein or polypeptide comprising the amino acid sequence of SEQ ID NO: 58 or (ii) a protein or polypeptide encoded by a nucleic acid molecule that hybridizes to the complement of SEQ ID NO: 57 under hybridization conditions comprising 1M Na^+ at 65° C. followed by wash conditions comprising 0.2× sodium citrate at 65° C. wherein the protein or polypeptide has ADP-ribosyl transferase activity.

2. The method according to claim **1**, wherein said introducing is carried out with the protein or polypeptide comprising the amino acid sequence of SEQ ID NO: 58.

3. The method according to claim **1**, wherein said introducing is carried out by transformation of the cell with a transgene encoding the protein or polypeptide.

4. The method according to claim **1**, wherein said introducing is carried out by delivery of the protein or polypeptide into the cell.

5. The method according to claim **1**, wherein the cell death pathway is suppressed.

* * * * *